16:43:54 2004

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GenCore v Copyright (c) 1993 -	GenCore version 5.1.6 c) 1993 - 2004 Compugen Ltd.		
OM protein - protein search, using sw model	w model		
Run on: October 1, 2004, 20:50:35	:50:35; Search time 128 Seconds (without alignments) 869.717 Million cell updates/sec	Seconds .s) .ll updates/sec	
Title: US-09-989-728-422 Perfect score: 2067 Sequence: 1 MFCPLKLILLPVLLDYSLGL	GLRNNSLEKKSGGGMPKTQQAF 394	IPKTQQAF 394	
Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	0.5		
Searched: 1586107 segs, 282547505 residues	505 residues		
Total number of hits satisfying chosen parameters:	en parameters: 1586107	.07	
Minimum DB seq length: 0 Maximum DB seq length: 200000000			
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	mmaries		
Database : A Geneseq 29Jan04:* 1: geneseqp1980s:* 2: geneseqp1990s:* 3: geneseqp2000s:* 5: geneseqp2001s:* 6: geneseqp2031s:* 7: geneseqp2033as:* 8: geneseqp2003bs:*			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES		
Result No.	Ö	Query Match	Length	DB	ID	Description	
-	2067	100.0	394	m	AAY66764	Aay66764 Membrane-	
۲۷	2067	100.0	394	m	AAB33454	Aab33454 Human PRO	
æ	2067	100.0	394	m	AAY94452	Aay94452 Human inf	
4	2067	100.0	394	m	AAB24433	Aab24433 Human PRO	
Ŋ	2067	100.0	394	4	AAU12431	Aau12431 Human PRO	
G	2067	100.0	394	4	AAM38860	Aam38860 Human pol	
7	2067	100.0		₹	AAB65287	Aab65287 Human PRO	
80	2067	100.0	394	Ŋ	AAU83689	Aau83689 Human PRO	
6	2067	100.0	394	Ŋ	ABB84933	Abb84933 Human PRO	
10	2067	100.0		S	ABB95539	Abb95539 Human ang	
11	2067	100.0	394	9	ABU58102	Abu58102 Human PRO	
12	2067	100.0		9	ABU59180	Abu59180 Novel hum	
13	2067	100.0	394	9	ABU82692	Abu82692 Human sec	
14	2067	100.0	394	9	ABO17875	Abol7875 Novel hum	
15	2067	100.0	394	ø	ABU60611	Abu60611 Human sec	
16	2067	100.0	394	v	ABU80836	Abu80836 Human PRO	
17	2067	100.0	394	9	AB033802	Abo33802 Novel hum	
1.8	2067	100.0	394	9	ABU13993	Abul3993 Human PRO	
19	2067	100.0	394	9	ABU81129	Abu81129 Human PRO	
20	2067	100,0	394	9	ABU72578	Abu72578 Novel hum	
21	2067	100.0	e	9	ABU66829	Abu66829 Human PRO	
22	2067	100.0	394	9	ABU59910	Abus9910 Novel sec	
23	2067	100.0	m	ø	ABU59327	Abu59327 Human sec	
24	2067	100.0		9	AB026024	Abo26024 Human PRO	
25	2067	100.0	e	9	AB025100	Abo25100 Human sec	

RESU	RESULT 1
AAY6	AAY66764
a	AAY66764 standard; protein; 394 AA.
XX	
AC	AAY66764;
X	
DI	05-APR-2000 (first entry)
×	
DE	Membrane-bound protein PRO1387.
X	
Κ¥	Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TII
¥	pharmaceutical; receptor immunoadhesin; gene mapping.
×	

E ligand;

98US-0087607P.
98US-0087621P.
98US-0088021P.
98US-0088021P.
98US-0088023P.
98US-008873P.
98US-008873P.
98US-008873P.
98US-0088773P.
98US-0088773P.
98US-0088773P.
98US-0088773P.
98US-0088773P.
98US-0088773P. 99WO-US012252. Homo sapiens. WO9963088-A2. 02-70N-1998 02-70N-1998 03-70N-1998 04-70N-1998 04-70N-1998 04-70N-1998 04-70N-1998 04-70N-1998 04-70N-1998 04-70N-1998 05-70N-1998 05-70N-1998 05-70N-1998 10-70N-1998 02-JUN-1999; 09-DEC-1999

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110998888888888888888888888888888888888	20000000000000000000000000000000000000	JUN-1998; JUN-1998; JUN-1998; JUN-1998; JUN-1998; JUN-1998; JUL-19
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The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors, TIE ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by recombinant techniques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goddard A, Gurney AL, Smith V, Watanabe CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 100.0%; Score 2067; DB 3; Length 394; Local Similarity 100.0%; Pred. No. 5.1e-188; es 394; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Membrane-bound proteins and related nucleotide sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 12; Fig 304; 822pp; English
98US-0095929P.
98US-00961146P.
98US-0096132P.
98US-0096132P.
98US-009673P.
98US-0096867P.
98US-0096867P.
98US-0096887P.
98US-0096887P.
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98US-0096897P.
98US-009699P.
98US-009699P.
98US-009797P.
98US-009797P.
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98US-009799F.
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Yuan J;
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                         11. AUG-1998

11. AUG-1998

17. AUG-1998

18. AUG-1998

18. AUG-1998

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26. AUG-1998
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Wood WI,
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The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematicus, rheumatoria arthritis, selected from systemic lupus erythematicsus, rheumatoria arthritis, systemic selected from systemic chronic arthritis, spondyloarthropathies, systemic selected in vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopeenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases, inflammatory bowel peripheral nervous systems, hepatobiliary diseases, inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, alloanmatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, allounding cor immune-mediated skin diseases, allergic disease, immunological diseases, fire rejection and graft-versus-host-disease. AACS6397 to AACS6598 cor represent PCR primers and hybridisation probes used in the isolation of human PRO polymucleotide and protein sequences given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGEHAKDEYVLYYYSNLSVPIGREQNRVHLMGDILCNDGSLLLQDVQEADQGTY1CEIRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
Tumas D, Watanabe CK, Wood WI, Yan M;
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                                                                         99WO-US021547.
99WO-US023089.
99US-0162506P.
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99WO-US030095.
99WO-US030999.
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2000WO-US000376.
2000WO-US003565.
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2000WO-US004342.
2000WO-US004414.
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99WO-US028564
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Best Local Similarity 100.0
Matches 394; Conservative
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                                                                                                                                                                                                                                                                                                                                           05-JAN-2000; 2
06-JAN-2000; 2
06-JAN-2000; 2
11-FEB-2000; 2
18-FBB-2000; 2
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01-SEP-1999
08-SEP-1999
13-SEP-1999
15-SEP-1999
15-SEP-1999
05-OCT-1999
29-OCT-1999
29-NOV-1999
30-NOV-1999
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20-DEC-1999;
30-DEC-1999;
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02-DEC-1999;
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                                       LVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVKKTC 300
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                                                                                                                                                                    IVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGN 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immune related disease; diagnosis; antiinflammatory;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rejection; graft-versus-host-disease.
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99US-0123618P.
99US-0123957P.
99US-0125775P.
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99US-0131445P.
99US-0132371P.
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99US-0144758P.
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10-MAR-1999;
12-MAR-1999;
23-MAR-1999;
12-APR-1999;
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04-MAY-1999;
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28-JUL-1999
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AAB33454
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180

240

240 300 300 360 360

120 180

120

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Gaps

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Human, PRO; promotion; inhibition; angiogenesis; cardiovascularisation; diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy; angiogenic; proliferative; cardiat; cardiovascular; antiatherosclerotic; cytostatic; gene therapy; vaccine.
                                                                                                                                                1 MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLS
                                                                                                                                                                                       61 PGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRL
                                                                                                                                                                                                         61 PGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRL
                                                                                                                                                                                                                                                  KGESQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEE
                                                                                                                                                                                                                                                                   181 IVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGN
                                                                                                                                                                                                                                                                                                                                  181 IVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGN
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                                                                                             0;
                                                              Length 394;
                                                                                             Indels
                                                             100.0%; Score 2067; DB 3;
100.0%; Pred. No. 5.1e-188;
ive 0; Mismatches 0;
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#11, derived from Incyte Clone 3507924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB24433 standard; protein; 394
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99US-0131445P.
99US-0134287P.
99US-0141037P.
99US-0144758P.
99US-0144758P.
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99US-0115554P.
99WO-US005028.
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                                                                            Best Local Similarity 100.
Matches 394; Conservative
                                 Sequence 394 AA;
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01-SEP-1999;
08-SEP-1999;
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12-JAN-1999;
08-MAR-1999;
12-MAR-1999;
28-APR-1999;
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                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eleven novel inflammation-associated genes have been identified in cDNA their coexpression with the Known inflammon selected according to their coexpression with the Known inflammon genes, CDIG, L-selectin, Src-like adapter protein, IP-30, superoxidase homoenzyme subunits, alpha-lantitypsin, Clq-A, S-lipoxygenses activating protein and SRC family tyrosine kinase. The novel polymucleotides may be used in hybridization assays to diagnose a disease or condition associated with altered useful in compositions for the diagnosis and treatment of such diseases associated with inflammation including rheumatoid arthritis, Crohn's diseases, multiple sclerosis, AIDS, diabetes mellitus, asthma and allergy. Additionally the polymucleotides of the invention may be used for gene therapy. The present sequence is human inflammation associated protein
                                                                                                                           240
                                                                                                                                                        LVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVKKTC 300
                                                                                                                                                                                                                    GNKSSVNSTVLVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEAT 360
                                                                                                                                                                                                                                     GHKSSVNSTVLVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEREEPSEKSEAT 360
PGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inflammation, rheumatoid arthritis, Crohn's disease; asthma, multiple sclerosis; allergy; AIDS; diabetes mellitus antiinflammatory; gene therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human inflammation-associated polypeptide useful for diagnosis, prevention and treatment of inflammatory diseases comprises product of gene coexpressed with e.g. CD16, L-selectin and IP-30.
                                                                                                                                                                         241 LVFKKTIVLHVSPEBEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVKKTC
                              KGESQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVPQSTBVKHVTKVBMIFSGRRAKEE
                                                 181 IVFRYYHKLAMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGN
                                                                                             181 IVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGN
                                                                                                                                                                                                                                                                               YMTMHPVWPSLRSDRNNSLEKKSGGGMPKTQQAF 394
                                                                                                                                                                                                                                                                                                       361 YMTMHPVWPSLRSDRNNSLEKKSGGGMPKTQQAF 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human inflammation associated protein #11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 42-43; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                        AAY94452 standard; protein; 394 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000-387787/33.
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Paoni NF;

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GNKSSVNSTVLVKOTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEAT 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 KGESQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVFWIFSGRRAKEE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGEHAKDBYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQBADQGTYICEIRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorders in mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGN
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                                                                                                       Hillan KJ;
Kuo SS, Pē
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 2067; DB 3;
100.0%; Pred. No. 5.1e-188;
tive 0; Mismatches 0;
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Klein RD,
Wood WI;
                                                                                                           , Ferrara N,
r, Gurney AL,
Williams PM,
                                                                                                                                                                                                                                                                   Claim 72; Fig 92; 315pp; English.
           99WO-US021090.
99WO-US021547.
99WO-US023089.
99US-0162506P.
99WO-US020944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             394; Conservative
                                                                                                                Baker KP,
                                                                                                                             Godowski PJ
                                                                                                                            Goddard A, Godowski P.
Smith V, Watanabe CK,
                                                                                   (GETH ) GENENTECH INC.
                                                                                                                                                                       WPI; 2000-412154/35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 394 AA;
                                                                                                                                                                                       N-PSDB; AAA77683
                                                                                                                   Ashkenazi AJ,
 13-SEP-1999;
15-SEP-1999;
15-SEP-1999;
05-OCT-1999;
                                                          29-OCT-1999;
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Best Local &
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Matches
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Isolated , secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumors e.g. lung,
                                                                              Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNP-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy.
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A, Godowski PJ, Gurney AL, Sherwood S;
tumas D, Watanabe CK, Wood WI, Zhang Z;
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                                                                   Human PRO1387 polypeptide sequence.
AAU12431 standard; protein; 394 AA.
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21-MAR-2000; 2000WO-US007532.
30-MAR-2000; 2000WO-US008439.
17-MAY-2000; 2000WO-US013705.
22-MAY-2000; 2000WO-US014042.
30-MAY-2000; 2000WO-US014941.
                                                                                                                                                                                                                                                                                                                                                                                 06-JAN-2000; 2000WO-US00376.

11-FBB-2000; 2000WO-US003451.

18-FBB-2000; 2000WO-US004342.

18-FBB-2000; 2000WO-US004342.

22-FBB-2000; 2000WO-US004414.

24-FBB-2000; 2000WO-US004914.

24-FBB-2000; 2000WO-US005014.

01-MAR-2000; 2000WO-US005811.

03-MAR-2000; 2000WO-US005811.

03-MAR-2000; 2000WO-US005811.

15-MAR-2000; 2000WO-US005811.

15-MAR-2000; 2000WO-US005811.

21-MAR-2000; 2000WO-US005811.
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2000WO-US030952
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99WO-US030999.
99WO-US031243.
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                                              (first entry)
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Smith V, Stev
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30-DEC-1999;
05-JAN-2000;
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20-DEC-1999;
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02-DEC-1999;
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                                              24-OCT-2001
                         AAU12431;
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Gaps

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Indels

RESULT 5 AAU12431

Length 394;

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amyotrophic lateral sclerosis, Shy-Drager Syndrome; chemotactic;
chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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25-APR-2000; 2000US-00552317.
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Zhou P, Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-442253/47.
N-PSDB; AAI58016.
                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                     WO200153312-A1
                                                                                                                                                                                                                                                      03-AUG-2000; 2
14-SEP-2000; 2
19-OCT-2000; 3
                                                                             Homo sapiens
                                                                                                                                                                                                                              20-JUN-2000;
19-JUL-2000;
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                                                                                                                                  26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                   Tang YT,
                     ANU12172-AAU12446 represent novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to mediate biological activities of cells expressing PRO polypeptides, to mediate biological activities of cells expressing PRO polypeptides expression in a coll sample to that in a control sample. Some necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or pericyte cells, the release of proteoglycans from carrilage, the proliferation or pericyte cells, the release of proteoglycans from expression in proliferation of conficeration of inner ear utricular supporting cells or of representation of inner ear utricular supporting cells or of reproliferation of inner ear utricular supporting cells or of repropried may modulate glucose or free faity acid uptake by skeletal (PMD) peptides may modulate glucose or free faity acid uptake by skeletal viroliseration of proliferation of endothelial cells or of repropried or by adhoryces, inhibit binding of A-peptide to factor convoluted in binding interactions. The POLYMOLGECIES modeling PRO colypeptides can be used in assays to identify molecules colls or knock out animals and can be used in gene therapy.
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                         Claim 12; Fig 520; 813pp; English.
  breast, prostate, cervical
                                                                                                                                                                                                                                                                                                                                                                                                Matches 394; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                             Sequence 394 AA;
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Zhao QA;

Wang D;

Ren F, Wa Zhang J,

Qian XB, Yang Y,

Ma Y, Xue AJ,

Chen R, rman T, Xu C, Drmanac RT;

Liu C, Asundi V, Yang Z, Wehrman T,

2000US-00598042; 2000US-00520312; 2000US-00653450; 2000US-0065191; 2000US-00633036; 2000US-00633036;

99US-00471275

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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM88642-AAM42213) with nootropic, encoded polypeptides (AAM88642-AAM42213) with nootropic, in gene therapy. A composition containing a polypeptide or polynucleotide in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous coff system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous system diseases, such as and calised neuropathy and central nervous system diseases, such as a lateral sclerosis, and Shy-brager Syndrome. Other uses include the cutilisation of the activity, chembracic/chemokinetic activity, haemostatic/chemokinetic activity, haemostatic/chemokinetic activity, haemostatic/chemokinetic activity, haemostatic/chemokinetic activity, haemostatic/chemokinetic activity, haemostatic/chemokinetic activity, arthritis and inflammation, leukaemias and corns assays for receptor activity, arthritis and inflammation, leukaemias and corns activity arthritis and inflammation, leukaemias and corns are activity activity and inflammation, leukaemias and corns activity arthritis and inflammation.
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Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 2067; DB 4; Length 394; 100.0%; Pred. No. 5.1e-188; tive 0; Mismatches 0; Indels 0;
                                                                                 Example 3; SEQ ID NO 2005; 10078pp; English.
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Matches 394; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 394 AA;
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Human, nootropic, immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

Human polypeptide SEQ ID NO 2005.

(first entry)

22-OCT-2001

AAM38860 standard; protein; 394 AA.

AAM38860

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Godowski PJ;
Paoni NF;
Wood WI;
                                      GNKSSVNSTVLVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEAT 360
                                                  LVEKKTIVLHVSBEEPRTLYTPAALRPLVLGGNOLVIIVGIVCATILLLPVLILIVKTC 300
                                                                                                                                                                                                                              Human; secreted and transmembrane protein; PRO; cytostatic; cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
                                                                                                                                                                                                              Human PRO1387 (UNQ722) protein sequence SEQ ID NO:422
                                                                                YMTMHPVWPSLRSDRNNSLEKKSGGGMPKTQQAF 394
                                                                                             AAB65287 standard; protein; 394 AA
                                                                                                                                                                                                                                                                                                                                                     99WO-US012252.
99US-0141037P.
99US-01443048P.
99US-0145698P.
99US-0145698P.
99US-0143946P.
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2000WO-US004914.
2000WO-US005004.
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2000WO-US003565.
2000WO-US004341.
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99US-0158663P.
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                                                                                                                                                                                                                                                      diagnostic assay
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11-FEB-2000;
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08-OCT-1999;
30-NOV-1999;
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28-JUL-1999;
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16-DEC-1999;
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15-SEP-1999
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PRO polynucleotides used to produce polypeptides used to target bioactive

N-PSDB; AAF44256

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The present invention describes human secreted and transmembrane PRO
proteins. The PRO proteins have cytostatic activity. The PRO proteins can
proteins. The PRO proteins have cytostatic activity. The PRO proteins can
cadiolables or antibodies, that cause cell death. PRO nucleotide
cadionables or antibodies, that cause cell death. PRO nucleotide
cancer, and their fragments, can be used as hybridisation probes, in
chromosomal and gene mapping, and in the generation of anti-sense RNA and
chromosomal and screen therapeutically useful reagents. The PRO nucleotide
concer. Anti-PRO antibodies can be used in diagnostic assays. ARF4420 to
cancer. Anti-PRO antibodies can be used in diagnostic assays. ARF4420 to
cancer. Anti-PRO sequences. ARF44087 to AAF44269 and AAB65134 to
isolation of human PRO sequences. ARF44087 to AAF44269 and AAB65154 to
the exemplification of the present invention
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molecules such as toxins, radiolabels or antibodies, to specific cells, to cause targeted cell death.
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0
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Best Local Similarity 100.0%; Pred. No. 5.1e-188;
Matches 394; Conservative 0; Mismatches 0;
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                                                       Claim 12; Fig 304; 935pp; English.
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                                                                                                                                                                                                                                                                                                                                           Sequence 394 AA;
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24-AUG-2000; 2000WO-US023328
10-NOV-2000; 2000WO-US0330873.
28-NOV-2000; 2000WO-US033646P
01-DEC-2000; 2000WO-US032678.
20-DEC-2000; 2000WO-US034956.
28-FRB-2001; 2010WO-US034956.
                                   2000US-0220585P.
2000US-0220605P.
2000US-0220607P.
2000US-0220624P.
                                                         2000US-0220638P.
2000US-0220664P.
                                                                    2000US-0220666P.
                 29-JUN-2001; 2001WO-US021066
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2000WO-US023522.
2000WO-US023328.
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                                                                                      2000US-0222425P
                                                                                                                                              01-MAR-2001; 2001WO-US006666
                                                             25-JUL-2000; 2
25-JUL-2000; 2
26-JUL-2000; 2
                                                                                    01-AUG-2000; 22-AUG-2000; 23-AUG-2000; 2
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10-MAY-2001;
      31-JAN-2002
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(GETH) GENENTECH INC.

Goddard A, Godowski PJ; phan JF, Watanabe CK, Wood WI; Gerritsen ME, Goddard Smith V, Stephan JF, Baker KP, Desnoyers L, Grimaldi JC, Gurney AL,

WPI; 2002-172001/22. N-PSDB; ABK33633. One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumors such as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or liver tumor.

Claim 11; Fig 196; 359pp; English.

The invention relates to one hundred and twenty two nucleic acids encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides cencode human secreted proteins. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating a PRO related disorder. The PRO polypeptides are useful for diagnosing tumours, especially lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour inversession of liver tumour. The PRO polypeptides are useful for stimulating the proliferation of or gene expression, in pericyte cells, for stimulating the release of tumour necrosis factor-alpha from human blood, for stimulating the proliferation of normal human blood, for stimulating or inhibiting the proliferation of normal human dermal weight markers and for tissue typing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, protein sequences of the invention.

Sequence 394 AA;

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                                           1 MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHYGDSALMGCVFQSTEDKCIFKIDWTLS
                                                          Gaps
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100.0%; Score 2067; DB 5; Length 394; 100.0%; Pred. No. 5.1e-188; ive 0; Mismatches 0; Indels 0;
                  Matches 394; Conservative
          Similarity
Query Match
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PGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRL 120
                                                                                                                                                     360
                                                                                                                                                                                                  Human; anglogenesis; cardiant; cytostatic; antianglogenic; hypotensive; vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; anglogenic disorder; cardiac hyportrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; rheumatoid arthritis; myocardial infarction; thrombophlebitis; lymphangitis; tumour anglogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping.
             KGBSQVFKKAVVIHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEE
                                                                                        IVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGN
                                                                                                       KGESQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEE
                                                                                                                                     LVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVKKTC
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                                                                                                                                                                                                                                            Human PRO1387 protein sequence SEQ ID NO:234.
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2001US-00767609.
2001US-00796498.
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2000US-0220624P.
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23-AUG-2000;
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18-SEP-2000;
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28-FEB-2001;
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cancer; disorder;

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301 GNKSSVNSTVLVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEAT 360
                                                                                                                                                                                                                                                                                         Human; angiogenesis; PRO protein; cardiovascularisation; wound; atherosclerosis; cardiac hypertrophy; gene therapy; endothelial cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic.
                                                                                                                                                                                                                                                              Human angiogenesis related protein PRO1387 SEQ ID NO: 234.
                                     361 YMTMHPVWPSLRSDRNNSLEKKSGGGMPKTQQAF 394
                                                           ABB95539 standard; protein; 394 AA
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22-JAN-2001; 2001US-00767609.
28-FEB-2001; 2001US-00796498.
28-FEB-2001; 2001WO-US006520.
01-MAR-2001; 2001WO-US006666.
14-MAR-2001; 2001US-008908689.
22-MAR-2001; 2001US-008916744.
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07-SEP-2000; 2000US-023328.

18-SEP-2000; 2000US-00664610.

18-SEP-2000; 2000US-00664610.

24-OCT-2000; 2000US-00709239.

08-NOV-2000; 2000US-00709238.

08-NOV-2000; 2000WO-US030873.

10-NOV-2000; 2000WO-US030873.

20-DEC-2000; 2000WO-US032678.

20-DEC-2000; 2000WO-US032678.
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2001US-00866034.
2001WO-US017092.
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10-MAY-2001; 2001US-00854208.
10-MAY-2001; 2001US-00854280.
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2001WO-US019692
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02-AUG-2000; 2000US-0222695P.
17-AUG-2000; 2000US-00643657.
23-AUG-2000; 2000WO-US023522.
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FERRARA N.
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(GODD/)
(GODO/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGEHAKDEYVLYYYSNLSVPIGRPQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                        One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
                                                                                                                                                                                                                                                                                                     , Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
JF, Watanabe CK, Williams PM, Wood WI, Ye W;
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100.0%; Pred. No. 5.1e-188;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Fig 234; 565pp; English.
                                                                            2001US-00816744.
2001US-00828366.
2001US-00854208.
2001US-00854280.
                                                                                                                                                                          25-WAY-2001; 2001WU-USU-12001WO-USU-130-WAY-2001; 2001WS-00870443.
                            2001WO-US006666.
2001US-00802706.
2001US-00808689.
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2001WO-US017092.
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Matches 394; Conservative
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                                                            14-MAR-2001; 2
22-MAR-2001; 2
05-APR-2001; 2
10-MAY-2001; 2
25-MAY-2001; 2
25-MAY-2001; 2
              28-FEB-2001;
01-MAR-2001;
09-MAR-2001;
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14-APR-2003 (first entry)
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25-FEB-1998;
20-MAR-1998;
28-APR-1998;
07-MAY-1998;
28-MAY-1998;
02-JUN-1999;
02-JUN-1999;
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                                                                                                                                                                                                                                                                                     The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atheroscierosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a PRO protein of the invention
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L, Hillan KJ, Marsters SA, Pan J, Paoni NF;
CK, Williams PM, Wood WI, Ye W;
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Matches 394; Conservative 0; Mismatches 0;
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                                                                                                                                     Godowski PJ, Gurney AL,
Stephan JF, Watanabe CK,
GURNEY A L.
HILLAN K J.
MARSTERS S A.
                                   PAN J.
PAONI N P.
STEPHAN J F.
WATANABE C K.
WILLIAMS P M.
                                                                                                                          Ferrara N,
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N-PSDB; ABL95677.
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         (HILL/)
(MARS/)
(PANJ/)
(PAON/)
                                                          (STEP/)
(WATA/)
(WILL/)
(WOOD/)
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ABU58102 standard; protein; 394 AA

ABU58102

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Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver; horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT; antibody-dependent enzyme mediated prodrug therapy.
                                                                                                                                      9705-0062130P

9705-0062130P

9705-0065118F

9705-0065118F

9805-0075945P

9805-008910P

9805-008910P

9805-0087607P

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9805-0089518P

9805-0089518P
                                                                                                               15-NOV-2001; 2001US-00997666
                Human PRO polypeptide #134
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18-JUN-1998;
19-JUN-1998;
19-JUN-1998;
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1S-0090355P 1S-0090429P 1S-0090431P 1S-0090444P 1S-0090444P 1S-0090451P 1S-0090535P 1S-009053P 1S-009057P 1S-0090678P 1S-0090678P 1S-0090678P 1S-0090678P 1S-009069P	98US-0090862P. 98US-0091863P. 98US-0091544P. 98US-0091473P. 98US-0091646P. 98US-0091628P. 98US-0091633P. 98US-0091633P. 98US-0091633P. 98US-0091633P. 98US-0091638P. 98US-0092182P. 98US-0092182P. 98US-0092182P. 98US-0092182P. 98US-0092333P. 98US-009531BP. 98US-009531BP. 98US-009531BP. 98US-009531BP. 98US-009531BP. 98US-009531BP. 98US-009531BP. 98US-009531BP. 98US-009531BP.	102 - 0.096 3.2 y (102 - 0.096 3.2 y (102 - 0.096 7.2 y (102 - 0.096 9.2 y (102 - 0.097 9
	26-JUN-1998; 26-JUN-1998; 01-JUL-1998; 02-JUL-1998; 02-JUL-1998; 02-JUL-1998; 02-JUL-1998; 02-JUL-1998; 02-JUL-1998; 03-JUL-1998; 07	- AUG-199
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241 LVFKKTIVLHVSPEBPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVKKTC 300

	Score 2067; DB 6; Pred. No. 5.1e-188; 0; Mismatches 0;
00000000000000000000000000000000000000	100.0%; Similarity 100.0%; 4; Conservative 0
26-AUG-1998; 11-AUG-1998; 16-SEP-1998; 17-SEP-1998; 17-SEP-1998; 17-SEP-1998; 01-DEC-1998; 01-DEC-1999; 02-JUN-1999; 02-JUN-1999; 02-JUN-1999; 02-JUN-1999; 02-JUN-1999; 03-JUN-1999; 03-JUN-1999; 04-DEC-1999; 05-JUN-1999; 06-JUN-1999; 06-JUN-1999; 06-JUN-1999; 06-JUN-1999; 06-JUN-1999; 06-JUN-1999; 07-DEC-1999; 01-DEC-1999; 01-DE	Query Match Best Local Simi Matches 394;
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Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
      98US-0088826P
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N-PSDB; ABX80392.
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06-JAN-2000;
11-FEB-2000;
18-FEB-2000;
22-FEB-2000;
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28-JUL-2000;
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24-AUG-2000;
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30-NOV-1999;
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16-DEC-1999;
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10-MAR-2000;
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Zhang Z;
     LVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVKKTC 300
                GNKSSVNSTVLVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVBEVIEEBEPSEKSEAT 360
                                                                                                                                                                             Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing; cardiac insufficiency disorder; cancer; tumour; immune response, adrenal cortical capillary endothelial growth; c-fos induction; vascular endothelial growth factor inhibition; veff inhibition; endothelial cell growth inhibitor; T-lymphocytes slimulation; retinal neurons cell survival; rod photoreceptor cell survival; retinal disorder; retinitis pigmentosum; kidney disorder; mammalian kidney mesangial cell proliferation; Berger disease; dermatitis; herpetiformis; Crohn's disease; chondrocyte redifferentiation; sports injury; arthritis.
                          Novel human secreted or transmembrane protein PRO1387,
                                                            361 YMTMHPVWPSLRSDRNNSLEKKSGGGMPKTQQAF 394
                                                     394
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                                                                                                              ABU59180 standard; protein; 394 AA
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97US-0062250P.
97US-0065311P.
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Godowski PJ;
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ong S, Gerber H, Gerritsen ME, Goddard A,
Gurney AL, Kljavin LJ, Napier MA, Pan J,
art TA, Tumas D, Watanabe CK, Williams PM,
980S-0088858P
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980S-0089105P
980S-0089512P
980S-0089532P
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Grimaldi JC, Gurney
Roy MA, Stewart TA,
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PRO1375, which stimulate proliferation of stimulated T-lymphocytes therapeutically useful for enhancing immune response and in cancer treatments.

Claim 12; Fig 304; 648pp; English

The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in linking a bioactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus useful for treating cardiac insufficiency disorders. PRO156, and PRO136, PRO43, PRO826, PRO166 or PRO535, PRO826, PRO816, PRO1360 and PRO1387 induce c-fos in endothelial growth, and are thus useful for treating canditions or disorders where angiogenesis would be eneficial, e-g. wound healing and antagonist of this polypeptide are useful for treating cancerous tumours. PRO812 inhibits vascular colled are useful for treating cancerous tumours. PRO812 inhibits vascular endothelial growth factor (VEGF) stimulated proliferation of endothelial growth factor (VEGF) stimulated proliferation of mammals which would be beneficial in inhibiting tumour growth. PRO826, PRO1046, PRO1144, PRO1346 and PRO1375 stimulated proliferation of stimulated T-lymphocytes and are therapeutically useful for renhancing immune response. PRO828, PRO826, PRO1068 or PRO10132 enhance survival of cretinal neurons cells (PRO1132 is also enhances survival/proliferation of disorders of injuries, e-g. retuinities pigmentosum, AMD. PRO819, PRO813 and therefore are useful for treating togenesses or other ephropathies associated with dermatitis, herpetiformis or Crohn's classase PRO1130, PRO814, PRO1132, PRO1192 and PRO116eration and/or redifferentiation of chondrocytes in culture and are thus useful for treating sports injuries, and arthritis. This is the amino acid sequence of a novel human PRO protein

Sequence 394 AA;

180 240 240 300 300 GNKSSVNSTVLVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEAT 360 PGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRL 120 61 PGEHAKDEYVLYYYSNLSVPIGREQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRL 120 180 9 9 121 KGESQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKBE IVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGN LVPKKTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVKKTC 181 IVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGN LVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVKKTC 1 MFCPLKLILLEPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLS 1 MFCPLKLILLEPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLS 0; Gaps 100.0%; Score 2067; DB 6; Length 394; 100.0%; Pred. No. 5.1e-188; Indels . YMTMHPVWPSLRSDRNNSLEKKSGGGMPKTQQAF 394 0; Mismatches Query Match Best Local Similarity 100. Matches 394; Conservative 301 361 241 301 121 181 g Ωp ò à qq ò g à d ò ⋧ a 8

Human secreted/transmembrane protein PRO1387 98US-0088126P. 98US-0088167P. 98US-0088212P. 98US-0088217P. 98US-008855P. 98US-0088734P. 98US-0088734P. 98US-0088810P. 98US-0088824P. 98US-0088858P. 98US-0088851P. 98US-0089105P. 98US-0089140P. 98US-008914PP. 98US-0089538P. 98US-0089598P. 98US-0089599P. 98US-0088029P. 98US-0088030P. 98US-0088033P. 98US-0087827P. 98US-0088021P. 98US-0088025P. 98US-0088026P. 97US-0065186P. 97US-0065311P. 97US-0066770P. 98US-0075945P. 98US-0078910P. 98US-0083322P. 98US-0084600P. 98US-0089532P 98US-0089801P 98US-0089907P 98US-0088028P 97US-0062250P. 97WO-US020069. 98US-0087106P 98US-0087607P 98US-0087609P 98US-0087759P 2001US-00990711 (first entry) US2003032023-A1 02-JUN-1998; 02-JUN-1998; 03-JUN-1998; 04-JUN-1998; 04-JUN-1998; 04-JUN-1998; 04-JUN-1998; 04-JUN-1998; 04-JUN-1998; 04-JUN-1998; 04-JUN-1998; 05-JUN-1998; 05-JUN-1998; 14-NOV-2001; 16-JUN-1997; 17-OCT-1997; 05-NOV-1997; 12-NOV-1997; 13-NOV-1997; Homo sapiens. 24-NOV-1997; 25-FEB-1998; 20-MAR-1998; 1998; 18-JUN-1998; 1998; 10-JUN-1998 10-JUN-1998; 1998 11-JUN-1998; 11-JUN-1998; 11-JUN-1998 12-JUN-1998 16-JUN-1998 7-JUN-1998 17-JUN-1998 17-JUN-1998 17-JUN-1998 17-JUN-1998 05-JUN-1998 05-JUN-1998 09-JUN-1998 10-JUN-1998 13-FEB-2003. 28-APR-1998 07-MAY-1998 28-MAY-1998 02-JUN-1998 26-JUN-2003 ABU82692; -NUL-01 10-JUN-10-JUN--NUL-91

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ABU82692 standard; protein; 394 AA.

Human, PRO; secreted protein, transmembrane protein, cardiac insufficiency disorders, angiogenesis, wound healing, cancerous tumour; immune response; retinal disorder; sight loss, retinitis pigmentosum; age-related macular degeneration; AMD; kidney disorder; Berger disease; nephropathy; dermatitis, herpetiformis; Crohn's disease; sports injury; arthritis.

98US-0089908P

RESULT 13 ABU82692

YMIMHPVWPSLRSDRNNSLEKKSGGGMPKTQQAF 394

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30S-0089947 30S-0089947 30S-00896248 30S-0090252 30S-0090252 30S-0090253 30S-0090435 30S-0090435 30S-0090445 30S-0090445 30S-0090445 30S-0090445 30S-0090445 30S-0090445 30S-0090645 30S-0090645 30S-0090646 30S-00906466 30S-00906466 30S-00906466 30S-00906466 30S-00906466 30S-009064666 30S-009064666666666666666666666666666666666	98US - 0090678P 98US - 0090690P 98US - 0090690P 98US - 0090696P 98US - 00906862P 98US - 0090863P 98US - 0091862P 98US - 0091819P 98US - 0091519P 98US - 0091519P 98US - 0091519P 98US - 009163P 98US - 009163P 98US - 009163P 98US - 009163P 98US - 009163P 98US - 009193P 98US - 009193P	US-00959161 US-0096121 US-0096121 US-0096131 US-0096131 US-0096131 US-0096721 US-0096721 US-0096721 US-0096731 US-0096891 US-0096891 US-0096891 US-0096891 US-0096891 US-0096891 US-0096891 US-0096891 US-0096891 US-0096891 US-0096891 US-0096891 US-0096891 US-0096891 US-0096891 US-0096891 US-0096891 US-0096891 US-0096950 US-0096950 US-0096950 US-009721 US-009721 US-009721 US-009721 US-009721 US-009721 US-009721 US-009721 US-009721 US-009721 US-009721
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PR 16-DEC-1999; 99US-018063P.
PR 17-MAR-2000; 2000WO-US00131S.
PR 17-MAR-2000; 2000WO-US00131S.
PR 23-MAY-2000; 2000WO-US0131S.
PR 23-

Query Match
Best Local Similarity 100.0%; Pred. No. 5.1e-188;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps

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 QY
 1 MFCPLKLILLPVILDYSIGLNDLNVSPPELTVHVGDSALMGCVPGSTEDKCIFKIDWTLS 60

 Db
 1 MFCPLKLILLPVILDYSLGLNDLNVSPPELTVHVGDSALMGCVPGSTEDKCIFKIDWTLS 60

 Cb
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 Cb
 61 PGEHAKDEYVLYYYSNLSVPIGREDNRVHLMGDILCNDGSLLLODVQBADGGTYICEIRL 120

 Cb
 61 PGEHAKDEYVLYYSNLSVPIGREDNRVHLMGDILCNDGSLLLQDVQBADGGTYICEIRL 120

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 121 KGBSQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEE 180

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IVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGN

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2001W0-US006666.
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2001US-0080689.
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01-MAR-2001;
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241 LVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVKTC 300
                                                                                         GNKSSVNSTVLVRNTKKTNPEIKERPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEAT 360
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 181 IVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGN 240
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98WO-US019177.
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14-MAY-1999;
02-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-SEP-1998;
14-SEP-1998;
14-SEP-1998;
16-SEP-1998;
17-SEP-1998;
29-OCT-1998;
29-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-NOV-1998
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08-MAR-1999
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                                                                                                                                                                                                                                        RESULT 14
                                                                                                                                                                                                                                                        ABO1787
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ABU60611 standard; protein; 394 AA.

01-MAY-2003

ABU60611;

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The invention describes an isolated nucleic acid (1) comprising, or which has 80 % sequence identity to, or the full-length coding sequence of, one of 275 nucleotide sequences, and which encodes a corresponding polypeptide selected from 275 amino acid sequences, where all sequences are given in the specification. The polypeptide encoded by (1) is used to detect the Optypeptide. Modulate a biological activity of a cell expressing a CR polypeptide, modulate a biological activity of a cell, stimulate the telease of tumour necrosis factor (TNP)-alpha from human blood, modulate the proliferation or differentiation of cells or gene expression, the uptake of glucose or free fatty acid by cells, stimulate or inhibit the proliferation or differentiation of cells or gene expression, stimulate the release of proteoglycans, stimulate the release of cytokine confident or differentiation of cells or gene expression.

Stimulate the release of proteoglycans, stimulate the release of cytokine confident or differentiation of cells or gene expression, confident or differentiation of cells or gene expression, confidentiation of acid and polypeptide encoded by it, are useful for treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, concert, or diaberic complications. The nucleic acid is useful as hybridisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KGESQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVFWIFSGRRAKEE 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLS 60
                                                                                                                                                                                                                                                   New secreted and transmembrane PRO nucleic acids, for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, axquired immunodeficiency
                  Filvaroff E, Gao W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVFKKTIVLHVSPEBPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVKKTC
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Beresini M, Deforge L, Desnoyers L, Filvaroff E, G, ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 12; Fig 520; 660pp; English.
                                                                                                                                                                                                                                                                                                                                                          syndrome (AIDS), or cancer.
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Matches 394; Conservative
                                                                                                                                            2003-341980/32.
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       Baker KP, Ber
Gerritsen ME,
                                                                                 Smith V,
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361

RESULT 15

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Human; PRO; secreted; transmembrane; signal peptide; pharmaceutical;
                                              Human secreted/transmembrane protein, #170
                                                                       diagnostic; therapeutic; gene therapy
                                                                                                                                                                       970S-0065311P

970S-0065311P

970S-0065311P

980S-0078910P

980S-0087106P

980S-0087106P

980S-0087106P

980S-0087106P

980S-0087105P

980S-0087105P

980S-0088028P

980S-0088028P

980S-0088028P

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980S-008812P

980S-008874P

980S-008876P

980S-008953P

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97WO-US020069
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                                                                                                    US2002160384-A1.
                                                                                      Homo sapiens.
                                                                                                                                 14-NOV-2001;
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is also available in electronic format from USPTO at segdata.uspto.gov/sequence.html

Sequence 394 AA;

88868

us-09-989-728-422.rag

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WPI; 2003-288106/28.
                      Roy MA,
Zhang Z;
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99WO-US025108.
99WO-US000106.
99WO-US012252.
99WO-US01290.
99WO-US021847.
99WO-US028313.
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15-MAR-2000;
20-MAR-2000;
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23-AUG-2000;
24-AUG-2000;
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(GETH) GENENTECH INC.

DL; Godowski PJ; Paoni NF; Wood WI; Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,

N-PSDB; ABX90370.

New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, as chromosome markers, or in generating probes.

Claim 12; Fig 304; 650pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides comprising a sequence without signal peptide and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide for linking a bioactive molecule to a cell expressing a PRO protein and for modulating at least molecule to a cell expressing a PRO protein and for modulating at least contained and properties or activity of a cell. The PRO pypeptides or polynucleotides are also useful in gene therapy, in chromosome dentification, as chromosome markers, or in generating probes. The PRO polymetides are useful as molecular markers for protein electrophoresis, and the isolated nucleic acids may be used for recombinantly expressing those markers. The PRO outibodies and nucleic acids may also be used in issue typing. Anti-PRO antibodies are useful in diagnostic assays for PRO, and in affinity purification of PRO from recombinant cell culture or natural sources. The sequences presented in ABUGO478-ABUG0624 are the PRO polymucleotides of the invention. Note: The sequence data for this patent

0 240 240 LVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVKKTC 300 GNKSSVNSTVLVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEAT 360 301 GNKSSVNSTVLVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEAT 360 120 120 180 180 09 09 IVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGN 241 LVPKKTIVLHVSPBEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLTLIVKKTC 61 PGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQBADQGTYICEIRL 1 MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLS 121 KGESQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEE 1 MECPLKLILLPVILDYSLGINDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLS 61 PGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRL Gaps · 0 Length 394; 0; Indels 100.0%; Score 2067; DB 6; 100.0%; Pred. No. 5.1e-188; iive 0; Mismatches 0; YMTMHPVWPSLRSDRNNSLEKKSGGGMPKTQQAF 394 YMTMHPVWPSLRSDRNNSLEKKSGGGMPKTQQAF 394 Search completed: October 1, 2004, 21:04:10 Job time : 135 8ecs Matches 394; Conservative Query Match Best Local Similarity 181 241 301 361 361 qq ò 쉱 g ઠ ò 셤 ò ò 셤 à qq

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04-70N-1998;
05-70N-1998;
05-70N-1998;
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04-JUN-1998;
04-JUN-1998;
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Aas77683 Human PRO
Aas21503 Human CDN
Aaf44256 Human PRO
Abk33633 CDNA enco
Ab188188 Human PRO
Abx77981 Human PRO
Abx80393 Novel hum
Acc69299 Human CDN
Acc69299 Human CDN
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thuman sec
CDNA enco
                                                                                       October 1, 2004, 19:36:10 ; Search time 943 Seconds (without alignments) 7343.121 Million cell updates/sec
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Novel
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Aaa21253 H
Aaa21253 H
Aba33633 6
Abb88188 H
Abb88188 H
Abb77981 H
Abx80393 N
Aca6929 H
Aca6929 H
Aca6938 Aca66938 Aca66938 Aca66938 Aca66898 Aca66898 Aca66898 Aca66898 Aca66898 Aca66898 Aca668216 Aca67253 Aca67253
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5.1.6
Compugen Ltd.
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                                                                                                                                                                                                                                                               3373863 seqs, 2124099041 residues
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GenCore version
Copyright (c) 1993 - 2004
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Maximum Match 100%
Listing first 45 summaries
                                                          OM nucleic - nucleic search, using sw model
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ACA69299
ACD24112
ABX90370
ACA66938
ACD68690
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ABL95677
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1630 7 ABX79577 1630 7 ACA93598 1630 7 ACA04283 1630 7 ACA93096 1630 8 ACA88484 1630 8 ACA88484 1630 8 ACA86463 1630 8 ADA1911 1630 8 ADA16469 1630 8 ADA16119 1630 8 ADA19119 1630 8 ADA19119	Abx79577 Human sec Aca93598 Novel hum Abx81280 Novel hum Aca04283 Human CDN	Novel Human Novel	CDNA e Novel Human	Human Human Homo s	CDNA Novel Human	Ada1/932 Human CUN Ada47897 Human PRO Ada21618 Human CDN Ada10405 Human CDN
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ALIGNMENTS

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Smith V, Watanabe CK;
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Yuan J;
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The invention provides membrane-bound PRO polypeptides and polymucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including ibL receptors, TIE ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunoadheeins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by recombinant techniques

U; 0 Other; Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0

0; Gaps Query Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1630; Conservative 0; Mismatches 0; Indels 0;

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ACACTGGCCCTGGGAACCAGGCTGAGTGGCTTCAAACCCCCCGTTGGATCAGACC
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ceggaagacercgaacacrogreaceceggeagecercaagacererggrerriggeresr
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                                                                                                                                                                                                                                                    Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorders in mammals.
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Kuo SS, Paoni
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Klein RD,
Wood WI;
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Pred. No. 0;
; Mismatches
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J, Gurney AL,
Williams PM,
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100.0%;
        99WO-US020111.
99WO-US020594.
99WO-US021090.
99WO-US021547.
99WO-US023089.
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Matches 1630; Conservative
                                                                                                                                                                Baker KP,
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                                                                                                                                                                             A, Goαυνω....
, Watanabe CK,
                                                                                                                                  (GETH ) GENENTECH INC.
                                                                                                                                                                                                                            2000-412154/35
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                                                                                                                                                               Ashkenazi AJ,
Goddard A, Go
Smith V, Wata
        01-SEP-1999;
08-SEP-1999;
13-SEP-1999;
15-SEP-1999;
15-SEP-1999;
05-OCT-1999;
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CTCCTGTGGGCAGGGTTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATAAAAACCAA 1620
ACACTGGCCCTGGGAACCAGGCTGAGCTGAGTGGCCTCAAACCCCCGTTGGATCAGACC 1560
                         Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy; ss.
                                                                                                                                                       Human cDNA sequence encoding for PR01387 polypeptide.
                                                                                                        AAS21503 standard; cDNA; 1630 BP
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                                                        CCCAAATCAA 1630
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18-FEB-2000;
22-FEB-2000;
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                                                                                                                                                                                                                Homo sapiens
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20-MAR-2000;
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AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO C polypeptides, to link bioactive molecules to cells expressing PRO C polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO C polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour cof ferentiation of chondrocytes, the proliferation or gene expression in dericty cells, the release of proteoglycans from cartilage, the proliferation of pericyte cells, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal colypeptides may modulate glucose or free fatty acid uptake by skeletal cursole cells or by adipocytes; or inhibit binding of A-peptide to factor involved in binding interactions. The polymucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, corresponding cor knock out animals and can be used in gene therapy
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                                                                                                                                                                                                    Isolated , secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumors e.g. lung,
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                                                            Desnoyers L, Filvaroff E, G:
PJ, Gurney AL, Sherwood S;
tanabe CK, Wood WI, Zhang Z;
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                                                          Deforge L, Desnoyers :
A, Godowski PJ, Gurne;
Tumas D, Watanabe CK,
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0; Mismatches
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                                                                                                                                                                                                                                                                       breast, prostate, cervical.
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                                                                                  Goddard
                   (GETH ) GENENTECH INC.
                                                            Beresini M,
                                                                                                 Stewart TA,
                                                                                                                                        WPI; 2001-408281/43.
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                                                                                Gerritsen ME,
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Matches 1630;
                                                            Baker KP,
                                                                                               Smith V,
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PRO polynuclectides used to produce polypeptides used to target bioactive molecules such as toxins, radiolabels or antibodies, to specific cells, to cause targeted cell death.
1501 ACACTGGCCCTGGGAACCAGGCTGAGCTGGCCTCAAACCCCCCGTTGGATCAGACC 1560
                              Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ; Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF; Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI; Zhang Z;
                                                                                                                                                                                                             Human; secreted and transmembrane protein; PRO; cytostatic; cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
                   CTCCTGTGGGCAGGGTTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATAAAAACCAA
                                                                                                                                                                                          SEQ ID NO:421
                                                                                                                                                                                            Human PRO1387 (UNQ722) nucleotide sequence
                                                                                                                                 BP.
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99US-0141037P
99US-0141037P
99US-014569BP
99US-014569BP
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99WO-US021090.
99WO-US021647.
99WO-US021647.
99WO-US021847.
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2000WO-US000376.
2000WO-US000376.
2000WO-US003565.
2000WO-US004341.
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2000WO-US005004.
2000WO-US005841.
2000WO-US006884.
                                                                                                                                  AAF44256 standard; cDNA; 1630
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26 - JUL - 1999;
17 - AUG - 1999;
15 - SEP - 1999;
16 - SEP - 1999;
30 - NOV - 1999;
30 - NOV - 1999;
30 - DEC - 1999;
16 - DEC - 1999;
20 - DEC - 1999;
20 - DEC - 1999;
21 - FEB - 2000;
22 - FEB - 2000;
24 - FEB - 2000;
26 - AMR - 2000;
27 - FEB - 2000;
28 - AMR - 2000;
29 - AMR - 2000;
20 - MAR - 2000;
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    GTGGAGTACTCCCAGAGCTGGGGCCACTTCCAGAATCGTGTGAACCTGGTGGGGGGACATT
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Claim 2; Fig 303; 935pp; English
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proteins. The PRO proteins have cytostatic activity. The PRO proteins can be used for targeted delivery of bloative molecules, such as toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used and protein sequence can be used for tissue typing and in treating and in treating and in treating and in treating and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to 1solation of human PRO sequences and hybridisation probes used in the AAB65300 represent human PRO polynucleotide and protein sequences as MAR44300 to EAR685300 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention present invention describes human secreted and transmembrane PRO seins. The PRO proteins have cytostatic activity. The PRO protein

Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other;

120 120 180 180 240 240 300 300 360 420 420 480 480 540 540 009 900 099 9 999 720 720 780 9 CGGCTCGAGTGCAGCTGTGGGAAGATTTCAGTGCATTGCCTCCCTGGGTGCTCTTCATC TTGGATTTGAAAGTTGAGAGCAGCATGTTTTGCCCCACTGAAACTCCATCCTGCTGCCAGTG TIGGATITGAAAGTIGAGAGCAGCAIGITTIGCCCCACTGAAACTCATCTGCTGCTGCCAGTG CATGTGGGTGATTCAGCTCTCTGATGGGGTTTTTCCAGAGCACAGAAGACAAATGTATA TTCAAGATAGACTGGACTCTGTCACCAGGAGGGCACGCCAAGGACGAATATGTGTATAC TTCAAGATAGACTGGACTCTGTCACCAGGAGAGCACGCCAAGGACGAATATGTGCTATAC TTACTGGATTATTCCTTGGGCCTGAATGACTTGAATGTTTCCCCGGCCTGAGCTAACAGTC CATGTGGGTGATTCAGCTCTGATGGGATGTTTTCCAGAGCACAGAGACAAATGTATA TATTACTCCAATCTCAGTGCCTATTGGGCGCTTCCAGAACCGCGTACACTTGATGGGG GACATCTTATGCAATGATGGCTCTCTCCTGCTCCAAGATGTGCAAAGAGGCTGACCAGGGA GACATCTTATGCAATGATGACTCTCCTGCTCCAAGATGTGCAAGAGGCTGACAGGGA **ACCTATATCTGTGAAATCCGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGT** ACCTATATCTGTGAAATCCGCCTCAAAGGGGAGGCCAGGTGTTCAAGAAGGCGGTGGTA ATGGGATGTGTTTTCCAGAGCACAGAAGTGAAACACGTGACCAAGGTAGAATGGATATTT TCAGGACGCCGCAAAGGAGGAGATTGTATTTCGTTACTACCACAAACTCAGGATGTCT GTGGAGTACTCCCAGAGCTGGGGCCACTTCCAGAATCGTGTGAACCTGGTGGGGGACATT TTCCGCAATGACGGTTCCATCATGCTTCAAGGAGTGAGGGAGTCAGATGAGGAGAAACTAC Gaps . 0 DB 5; Length 1630; Indels ó 100.0%; Score 1630; 100.0%; Pred. No. 0; iive 0; Mismatches Best Local Similarity 100. Matches 1630; Conservative 61 Query Match 61 121 121 181 181 241 241 301 301 361 361 541 421 121 481 481 541 601 601 661 661 721 Db g ò ò g à a ò à g δ d δ qq ò

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cDNA encoding human PRO protein, Seq ID No 195.

(first entry)

08-MAY-2002

XEXH

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ζ	781 ACCTGCAGTATCCACCTAGGGAACCTGGTGTTCAAGAAAACCATTGTGCTAGCATGTCAGC	840
qα	781 ACTGCAGTATCCACCTAGGGAACCTGGTGTTCAAGAAAACCATTGTGCTGCATGTCAGG	840
67		900
qa	841 CCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGGCCTCTGGTGGGTG	900
<i>\</i> ∂	901 AATCAGTGGTGATCATTGTGGGAATTGTCTGTGCCACAATCCTGCTGCTGCTCCTGTTCTG 9	096
QQ	6	096
δλ	961 ATAITGAICGIGAAGACCIGIGGAAATAAGAGIICAGIGAAITCIACGICIIGGIG 1	
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٥y	1021 AAGAACACGAAGAAGACTAATCCAGAGATAAAAGAAAAACCTGCCATTTTGAAAGATGT 10	1080
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ò	1081 GAAGGGAGAAACACATTTACTCCCCAATAATTGTACGGGAGGTGATCGAGGAAGAA 1:	1140
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qa	CAAGTGAAAAATCAGAGGCCACCTACATGACCATGCACCAGTTTGGCCTTCTGAGG	2
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qq	CAGATCGGAACAACTCACTTGAAAAAAGTCAGGTGGGGGAATGCCAAAAACACACAGA	56
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Ob	1261 GCCTTTTGAGAAGAATGGAGAGTCCCTTCATCTCAGCAGCGGTGGAGACTCTCTCCTGTG 13	32
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qq	21 TGTGTCCTGGGCCACTCTACCAGTGATTTCAGACTCCCGGCTCTCCCAGCTGTCTCTT 1	3
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qa	01 ACACTGGCCTGGGAACCAGGCTGAGTGGGCCTCAAACCCCCCGTTGGATCAGACC 1	
ò	1 CTCCTGTGGGCAGGGTTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATAAAAACCAA 1	620
qa	Н	620
δλ	1621 CCCAAATCAA 1630	
đ	1621 CCCAAATCAA 1630	
RESULT ABK336	533	
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S X E	ABK33633;	

Length 1630;

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(GETH ) GENENTECH INC.
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cancer; colon cancer;
              breast cancer; prostate tumour; rectal tumour; liver tumour; pericyte cell proliferation; chondrocyte cell proliferation; tumour necrosis factor-alpha; gene; ss.
 secreted protein; PRO; tumour; lung
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2000US-0220666P.
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28-FEB-2001;
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01-AUG-2000;
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• hundred and twenty two nucleic acids encoding PRO polypeptides, ful for treating a PRO related disorder and for diagnosing tumors such lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor liver tumor. Godowski PJ; مع Wood WI; Watanabe CK, Goddard A, Gerritsen ME, Goddard Smith V, Stephan JF, L, AL, Desnoyers C, Gurney WPI; 2002-172001/22. P-PSDB; AAU83689. Grimaldi JC,

Claim 2; Fig 195; 359pp; English.

The invention relates to one hundred and twenty two nucleic acids encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides encode human secreted proteins. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating a PRO related disorder. The PRO polypeptides are useful for diagnosing tumours, percent disorder. The PRO polypeptides are useful for diagnosing tumours, rectal tumour or liver tumour. The PRO polypeptides are useful for stimulating the proliferation of, or gene expression, in periorte cells, for stimulating the release of tumour necrosis factor-alpha from human blood, constituing the release of tumour necrosis factor-alpha from human blood, constituing the proliferation of normal human blood, consideration of ninhibiting the proliferation of normal human blood, considerations and for tissue typing, The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping, ABK313657 represent human PRO protein coding sequences of the invention

BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other; Sequence 1630

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1021 AAGAACACGAAGAAGACTAATCCAGAGATAAAAGAAAAACCCTGCCATTTTGAAAAGATGT 1080
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                                              CGGCTCGAGTGCAGCTGTGGGAGATTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATC
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100.0%; Score 1630; 100.0%; Pred. No. 0;
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Query Match
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Matches 1630; Conservative
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10-NOV-2000; 2000MO-US030952. 10-NOV-2000; 2000MO-US030952. 01-DEC-2000; 2000MO-US032678. 20-DEC-2000; 2000US-00747259. 20-DEC-2000; 2000WO-US032678.

2000WS-0222695P. 2000WS-00643657. 2000WO-US023522. 2000WO-US023328. 2000WS-0230978P.

02-AUG-2000; 17-AUG-2000; 23-AUG-2000; 24-AUG-2000;

2000US-00664610. 2000US-00665350. 2000US-0242922P.

07-SEP-2000; 2 18-SEP-2000; 2 18-SEP-2000; 2 24-OCT-2000; 2

08-NOV-2000; 08-NOV-2000;

20-DEC-2000; 2000WO-USO34956. 22-JAN-2001; 2001US-00796498. 28-FEB-2001; 2001US-00796498. 28-FEB-2001; 2001WO-USO06665. 01-MAR-2001; 2001US-00802706. 14-MAR-2001; 2001US-00808689. 22-MAR-2001; 2001US-0081644.

10-MAY-2001; 2001US-00854208. 10-MAY-2001; 2001US-00854280. 25-MAY-2001; 2001US-00866028. 25-MAY-2001; 2001US-00866034.

25-MAY-2001; 30-MAY-2001; 01-JUN-2001; (GETH) GENENTECH INC.

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Human PRO1387 cDNA sequence SEQ ID NO:233.
                                BP
                           ABL88188 standard; cDNA; 1630
                                                                                         (first entry)
                                                                                        16-MAY-2002
                                                           ABL88188;
                ABL88188
RESULT
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Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; rheumatoid arthritis; myocardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping; gene; ss. WO200200690-A2 Homo sapiens 03-JAN-2002

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                                                                   1 CGGCTCGAGTGCAGCTGTGGGGAGATTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATC
                                                                                          1 CGGCTCGAGTGCAGCTGTGGGGAGATTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATC
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   DB 6; Length 1630;
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                Best Local Similarity 100.
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                                                                       23-JUN-2000; 2000US-0213637P.
20-JUL-2000; 2000US-0219556P.
                                      20-JUN-2001; 2001WO-US019692
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ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic, antianglogenic, hypotensive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polynucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABL88259 to ABL88257 represent primers and probes used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Paoni NF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J,
Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goddard A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Fig 233; 565pp; English.
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1141 CCAAGTGAAAAATCAGAGGCCACTACATGACCATGCTCCTTTTGGGTTTTTTTT	RESULT 7 ABL95677 XX XX C ABL95677; XX C ABL95677; XX Human angiogenesis related cDNA PRO1387 SEQ ID NO: 233. XX Human angiogenesis, PRO protein; cardiovascularisation; wound; cancer; XX Human; angiogenesis, PRO protein; cardiovascularisation; wound; cancer; XX Human; angiogenesis, pRO protein; cardiovascularisation; wound; cancer; XX Human; angiogenesis, pRO protein; cardiovascularisation; wound; cancer; XX Matherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder; XX How sapiens. XX How sapiens. XX
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TTGGATTTGAAAGTTGAGAGCAGCATGTTTTGCCCACTGAAACTCATCCTGCTGCCAGTG TTGGATTTGAAAGTTGAGAGCAGCATGTTTTGCCCACTGAAACTCATCCTGCTGCCAGTG TTGGATTTGAAAGTTGAGAGCAGCATGTTTTCCCCACTGAAACTCATCCTGCTGCTGCTGCTAACAGTC TTACTGGATTATTCCTTGGGCCTGAATGACTTGAATGTTTTCCCCGCCTGAGCTAACAGTC TTACTGGATTATTCCTTGGGCCTGAATGACTTGAATGTTTTCCCGGCCTGAGCTAACAGTC TTACTGGATTATTCCTTGGGCCTGATGGGATGTTTTTCCCGGCCTGAGCTAACAGTC TTCAAGATTAACTCCAGCTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATA TTCAAGATTAGACTGGACTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATA TTCAAGATTAGACTGGACTCTGTCACCAGGAGAGCACAGAAGACAAATGTATA TTCAAGATTAGACTGGACTCTGTCACCAGGAGAGCACAGAAGACAAATGTATA TTCAAGATTAGCATGTGACCAGGAGAGCACCAAGGACCAAAATGTATACAGAATACTCCAATCTCAAGATAGAT	TCAGGACGCGCAAAGGAGGATTGTATTTCGTTACTACCACAAACTCAGGATCAGGACGCGCGCAAAGGAGGAGATTGTATTTCGTTACTACCACAAACTCAGGATCAGGACGCGCGCG

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Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other;
08-NOV-2000; 2000WO-US030952.
10-NOV-2000; 2000WO-US030873.
01-DBC-2000; 2000WO-US032678.
20-DBC-2000; 2000WO-US032678.
20-DBC-2000; 2000WO-US034956.
22-JAN-2001; 2001WS-0076769.
28-FEB-2001; 2001WS-00796498.
28-FEB-2001; 2001WS-0080665.
09-MAR-2001; 2001WS-0080689.
14-MAR-2001; 2001WS-0080689.
22-MAR-2001; 2001WS-0080689.
10-MAY-2001; 2001WS-00854208.
10-MAY-2001; 2001WS-00854208.
25-MAY-2001; 2001WS-00866028.
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30-MAY-2001; 2001US-00870574.
30-MAY-2001; 2001US-00870574.
01-UJN-2001; 2001WO-US017800.
20-JUN-2001; 2001WO-US019692.
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BAKER K P.
FERRARA N.
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GODOWSKI P J.
GURNEY A L.
HILLAN K J.
MARSTERS S A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GERBER H.
GERRITSEN M E.
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STEPHAN J F.
WATANABE C K.
WILLIAMS P M.
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P-PSDB; ABB95539.
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PAONI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baker KP,
Godowski P
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(MARS/)
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    RAHARAHAH KANAMENTAN K
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The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenois, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal. Paoni NF coding sequence of the invention Gerber H, Gerritsen ME, Goddard A, J, Hillan KJ, Marsters SA, Pan J, TK, Williams PM, Wood WI, Ye W, The present sequence is a Claim 1; Fig 233; 567pp; English. Watanabe CK, AL,

ö 9 cedericeAerideAeridieGeGAGATTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATC CGGCTCGAGTGCAGCTGTGGGGAGATTTCAGTGCATTGCCTCCCTGGGTGCTCTTCATC Gaps . 0 DB 6; Length 1630; 0; Indels llarity 100.0%; Score 1630; Conservative 0; Mismatches Local Similarity Les 1630; Conserv Query Match Matches ર્જ g

TIGGATITIGAAAGTIGAGAGCAGCAIGTITIGCCCACTGAAACTCAICCTGCTGCCAGTG 120

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1020 180 180 240 CCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCCCCCAGTTTGGCCTTCTCTGAGG 1200 300 300 360 360 420 540 420 480 480 540 009 600 099 720 780 096 720 780 840 840 900 TTCAAGATAGACTGGACTCTGTCACCAGGAGAGCACGCCAAGGACGAATATGTGCTATAC TIGGATITIGAAAGITIGAGAGCAGCATGITITIGCCCACTGAAACTCCTGCTGCTGCCAGTG TTACTGGATTATTCCTTGGGCCTGAATGACTTGAATGTTTCCCCGCCTGAGCTAACAGTC 121 TTACTGGATTATTCCTTGGGCCTGAATGACTTGAATGTTTCCCCGCCTGAGCTAACAGTC CATGTGGGTGATTCAGCTCTGATGTGTTTTTCCAGAGCACAGAAGACAAATGTATA CATGTGGGTGATTCAGCTCTGATGGGATGTGTTTTCCAGAGCCACAGAAGACAAATGTATA TTCAAGATAGACTGGACTCTGTCACCAGGAGAGCACGCCCAAGGACGAATATGTGCTATAC TATTACTCCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGGCGTACACTTGATGGGG GACATCTTATGCAATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACGAGA GACATCTTATGCAATGATGGCTCTCTCTGCTCCAAGATGTGTGCAAGAGGCTGACGGGA ACCTATATCTGTGAAATCCGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGTA crecarerecriceagagageceaaagageceareaegaecareregagarreae ATGGGATGTGTTTTCCAGAGCACAGAAGTGAAACACGTGACCAAGGTAGAATGGATATTT 541 AIGGGAIGTGTTTTCCAGAGCACAGAAGTGAAACACGTGACCAAGCTAGAAIGGATATTT TCAGGACGCGCGCAAAGGAGGAGATTGTATTTCGTTACTACCACAACTCAGGATGTCT GTGGAGTACTCCCCAGAGCTGGGGCCACTTCCAGAATCGTGTGAACCTGGTGGGGGACATT TTCCGCAATGACGGTTCCATCATGCTTCAAGGAGTGAGGGAGTCAGATGGAGGAAACTAC ACCTGCAGTATCCACCTAGGAACCTGGTGTTCAAGAAAACCATTGTGCTGCATGTCAGC TCAGGACGCCCCAAAGGAGGAGATTGTATTTCGTTACTACCACAAACTCAGGATGTCT GTGGAGTACTCCCAGAGCTGGGGCCACTTCCAGAATCGTGTGAACCTGGTGGGGGACATT CCGGAAGACCTCGAACACTGGTGACCCCGGCAGCCCTGAGGCCTCTGGTCTTGGGTGGT AATCAGTIGGIGATCATIGIGGGAATIGICIGIGCCACAATCCTGCTGCTCCTCTGTTCTG AATCAGTTGGTGATTGTGGGAATTGTCTGTGCCACAATCCTGCTGCTCCCTGTTCTG **ATATTGATCGTGAAGAAGACCTGTGGAAATAAGAGTTCAGTGAATTCTACAGTCTTGGTG AAGAACACGAAGAAGACTAATCCAGAGATAAAAGAAAAACCCTGCCATTTTGAAAGATGT** AAGAACACGAAGAAGACTAATCCAGAGATAAAAGAAAAACCCTGCCATTTTGAAAGATGT GAAGGGGAGAAACACATTTACTCCCCAATAATTGTACGGGAGGTGATCGAGGAAGAA 121 181 181 241 241 301 301 361 361 421 481 541 421 481 601 199 781 601 721 721 781 841 901 1021 1021 1081 1141 661 901 961 961 1081 d ò g 8 ò g ò 셤 δ g à g ò g ò g à a g ò 셤 엄 g δ à 8 ò g à g ò g ∂ 유

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Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing; cardiac insufficiency disorder; cancer; tumour; immune response; adrenal cortical capillary endothelial growth, c-fos induction; vascular endothelial growth factor inhibition; VEGF inhibition; retinal cell growth inhibitor; T-lymphocytes stimulation; retinal heurons cell survival; rod photoreceptor cell survival; retinal disorder; retinitis pigmentosum; kinhey disorder; meanmalian kidney mesangial cell proliferation; Berger disease; dermathtis; herpetiformis; Crohn's disease; chondrocyte proliferation; chondrocyte redifferentiation; sports injury; arthritis; gene; ds.
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(GETH) GENENTECH INC.

DL; Godowski PJ; Paoni NF; Wood WI; Eaton Baker KP, Botstein D, Desnoyers L, Eaton ong S, Gerber H, Gerritsen ME, Goddard A, Gurney AL, Kljavin IJ, Napier MA, Pan J, art TA, Tumas D, Watanabe CK, Williams PM, Ashkena... Ferrara N, Fony Grimaldi JC, Gurney Al

WPI; 2003-247083/24.

P-PSDB; ABU59181

il isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 PRO1375, which stimulate proliferation of stimulated T-lymphocytes therapeutically useful for enhancing immune response and in cancer treatments Novel and are

Claim 2; Fig 305; 648pp; English

The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in polypeptides are useful in detecting PRO polypeptides in a sample, in inking a bioactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus useful for treating cardiac insufficiency disorders. PRO1584 and PRO1186 stimulate adrenal cortical capillary endothelial growth, and PRO136, PRO943, PRO943, PRO926, PRO1068 or PRO535, PRO926, PRO919, PRO1367, PRO1367 induce c-fos in endothelial cells, and are thus useful for treating conditions or disorders where angiogenesis would be beneficial, e.g. wound healing and antagonist of this polypeptide are useful for treating cancerous tumours. PRO912 inhibits vascular condothelial growth factor (VEGP) stimulated proliferation of endothelial cells and is thus useful for inhibiting endothelial cell growth, in mammals which would be beneficial in inhibiting rumour growth.

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ö ð 240 120 180 180 240 TTCAAGATAGACTGGACTCTGTCACCAGGAGCACGCCAAGGACGAATATGTGCTATAC 300 300 TATTACTCCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGCGTACACTTGATGGGG 360 360 420 420 480 480 540 540 600 900 099 099 720 720 9 stimulated T-lymphocytes and are therapeutically useful for enhancing immune response. PRO828, PRO826, PRO1068 or PRO132 enhance survival of retinal neurons cells (PRO132 is also enhances survival/proliferation crod photoreceptor cells) and therefore are useful for treating retinal disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813 and PRO11066 induce proliferation of mammalian kidney mesangial cells, and therefore are useful for treating kidney disorders associated with decreased mesangial cell function such as Berger disease or other nephropathies associated with dermatitis, herpetiformis or Crohn's disease. PRO110, PRO844, PRO1112, PRO1192 and PRO1387 induce the proliferation and/or redifferentiation of chondrocytes in culture and ar thus useful for treating sports injuries, and arthritis. This sequence represents a novel human PRO protein polynucleotide CATGTGGGTGATTCAGCTCTGATGGGATGTTTTTCCAGAGCACAGAGACAAATGTATA CATGTGGGGTGATTCAGCTCTGATGGGATGTTTTTCCAGAGCACAGAAGACAAAATGTATA TTACTGGATTATTCCTTGGGCCTGAATGACTTGAATGTTTCCCCGCCTGAGCTAACAGTC TTCCGCAATGACGGTTCCATCATGCTTCAAGGAGTGAGGGAGTCAGATGGAGGAAACTAC cescriceasracascristessasarrreasrecarrecerecereserecreare 61 TIGGATITIGAAAGTIGAAGCAGCAIGTITIGCCCACTGAAACTCCATGCTGCCAGTG 241 Trcaagaragacrecrescenceagagagacacceaagaacaaragaaragacrarac TATTACTCCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGCGTACACTTGATGGGG GACATCITATGCAATGATGGCTCTCTCTGCTCCAAGATGTGTGCAAGAGGCTGACCAGGGA ACCTATATCTGTGAAATCCGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTA TCAGGACGGCGCGCAAAGGAGGAGTTGTATTTCGTTACTACCACAAACTCAGGATGTCT 1 CGGCTCGAGTGCAGCTGTGGGGAGATTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATC GACATCTTATGCAATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGA ACCTATATCTGTGAAATCCGCCTCAAAGGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTA crecargrectriccaeaeaeaecccaaaeacrcargerccargreegeagarrcae ATGGGATGTGTTTTCCAGAGCACAGAAGTGAAACACGTGACCAAGGTAGAATGGATATTT ATGGGATGTTTTCCAGAGCACAGAAGTGAAACACGTGACCAGGTAGAATGGATATTT TCAGGACGCCCCCAAAGGAGGAGATTGTATTTCGTTACTACCACAAACTCAGGATGTCT GTGGAGTACTCCCAGAGCTGGGGCCACTTCCAGAATCGTGTGAACCTGGTGGGGGACATT Greengracticccaeaecreeccacriccaeaarcereaaccreereagaecarr Gaps PRO1184, PRO1346 and PRO1375 stimulate proliferation of . 0 Length 1630; Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other; Indels . DB 7; 0; Mismatches Score 1630; Pred. No. 0: 100.0%; Best Local Similarity 100. Matches 1630; Conservative 61 121 181 181 301 541 Query Match 301 361 361 421 421 481 481 541 601 501 561 721 ò g ઠે g ð g ò 엄 à g ò g ò g à 엄 à οp ò ద g d $\dot{\delta}$ ò

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cancerous tumour; immune response; retinal disorder; sight loss; retinitis pigmentosum; age-related macular degeneration; AMD; kidney disorder; Berger disease; nephropathy; dermatitis; herpetiformis; Crohn's disease; sports injury; arthritis.
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QY 361 GACATCTTATGCAATGATGGCTCTCCCTGCTCCAAGATGCAAGAGGCTGACCAGGGA 420 Db 361 GACATCTTATGCAATGATGGCTCTCCCTGCTCCCAAGATGTGCCAAGAGGCTGACCAGGGA 420 Sb 421 ACCTATATCTGTGAAATCCGCCTCAAAGAGGCCAGGTGTTCAAGAAGGCGGTGGTA 480 CD 421 ACCTATATCTGTGAAATCCGCCTCAAAGAGGCCAGGTGTTCAAGAAGGCGGTGGTA 480 CD 481 CTGCATGTGATATCTGTGAAATCCGCCTCAAAGAGGCCAAGGTGTTCAAGAAGGCGGTGGTA 480 CD 481 CTGCATGTGTTCCAGAGGAGCCCAAAGAGCTCATGGTCCATGTGGGTGG	TCAGGACGCCCCAAAGGAGATTGTATTTCGTTACTACCACAAACTCAGGATGTCT TCAGGACGCCGCCAAAGGAGAGATTGTATTTCGTTACTACCACAAACTCAGGATGTCT CTAGGACGCCGCCACAGGAGAGATTGTATTTCGTTACTACCACAAACTCAGGATGTCT GTGGAGTACTCCCAGAGTGGTGGGGCCACTTCCAGAATCGTGTGAACCTGGTGGGGGACATT GTGGAGTACTCCCAGAGCTGCGGGCCACTTCCAGAATCGTGTGAACCTGGTGGGGGACATT GTGGAGTACTCCCAGAGCTGCATCAACATCAAGAGGAAACTAC	TCCGCAATGACGGTTCCATCATGCTTCAAGAGTGAGGGGAGTCAGATGGAGGGAAACTAC ACCTGCAGTATCCACCTAGGGAACCTGGTGTTCAAGAAAACCATTGTGCTGCATGTCAGC ACCTGCAGTATCCACCTAGGGAACCTGGTGTTCAAGAAAACCATTGTGCTGCATGTCAGC CCGGAAGAGCCTCGAACACTGGTGTTCAAGAAAACCTTGTGCTGCATGTTCAGC CCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGGCCTTGGGTGGT CCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGGCCTTTGGGTGGT CCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGGCCTTTGGGTGGT CCGCAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTTGAGGTCTTTGGGTGGT	901 AATCAGTTGGTGATCATTGTGGGAATTGTCTGTGCCACAATCCTGCTGCTCCTGTTCTG 960	1021 AAGAACGCGAAGAAGCCTAAACCAGCATTTTGAAAGATGT 1080 1021 AAGAACACGAAGATGT 1080 1021 AAGAACACGAAGAAACCCTGCCATTTTGAAAGATGT 1080 1081 GAAGGGGAGAAAACCCTGCCATTTTGAAAGATGT 1080 1081 GAAGGGGAGAAAACATTTACTCCCCAATAATTGTACGGGAGGAGAAGAAAA 1140 1161	1141 CCAAGTGAAAATCAGAGGCCACCTACATGACCATGCACCCCAGTTTGGCCTTCTGAGG 1200	1261 GCTTTTGAGAAGAATGGAGAGCCCTTCAGCGGGGGGGGCGCTCCTCTGTG 1320 1321 TGTGTCCTGGGCCCCTTCACCAGTGATTTCAGACTCCCGCTCTCCCAGTGTCCTCTGTG 1320 1321 TGTGTCCTGGGCCACTCTACCAGTGATTTCAGACTCCCGCTCTCCCAGCTGTCCTCTT 1380 1321 TGTGTCCTGGGCCACTCTACCAGTGATTTCAGACTCCCGCTCTCCCAGCTGTCCTCTT 1380 1381 GTCATTGTTTGGTCAATACACTGAAGATTGGAGAATTTGGAGCCTGGCAGAAGACTGGAC 1440 1381 CTCATTGTTTGGTCAATACACTGAAGATGGAGAAATTTGGAGCCTGGCAGAAGACTGGAC 1440 1441 AGCTCTGGAAGAACAGGCCTGCTGAAGAGAGAGACTTGGCCTCTGGAACTGGAC 1450

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The invention describes an isolated mucleic acid (1) comprising, or which has 80 % sequence identity to, or the full-length coding sequence of, one of 275 mucleotide sequences, and which encodes a corresponding code of 275 mucleotide sequences, and which encodes a corresponding polypeptide selected from 275 amino acid sequences, where all sequences are given in the specification. The polypeptide encoded by (1) is used to detect PRO polypeptide, modulate a biological activity of a cell, stimulate the PRO polypeptide, modulate a biological activity of a cell, stimulate the release of tumour necrosis factor (TNF)-alpha from human blood, modulate the proliferation or differentiation of cells or gene expression, the proliferation or differentiation of cells or gene expression, confirm paripheral blood enconuclear cells, inhibit the binding of A-peptide from paripheral blood enconuclear cells, inhibit the binding of A-peptide of acid and polypeptide encoded by it, are useful for treating inflammatory diseases, organ failure, atherence of tumour in a mammal. The nucleic cofficences, premature aging, acquired immunodeficiency syndrome (AIDS), cancer, or diabetic complications. The nucleic acid is useful as hybridisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful in tissue apping. This sequence encodes a novel human secreted and transmembrane PRO ô New secreted and transmembrane PRO nucleic acids, for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, axquired immunodeficiency Gao W; CGGCTCGAGTGCAGCTGTGGGAGATTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATC Gaps Deforge L, Desnoyers L, Filvaroff E, G. A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z; . 0 DB 7; Length 1630; Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other; Indels ., 100.0%; Score 1630; 100.0%; Pred. No. 0; tive 0; Mismatches Claim 2; Fig 519; 660pp; English. syndrome (AIDS), or cancer. Best Local Similarity Matches 1630; Conservative Beresini M, Goddard ME, Goddard Stewart TA, WPI; 2003-341980/32. P-PSDB; ABO17875. Query Match Best Local Similarity polypeptide Gerritsen Smith V,

240 180 180 240 TIGGATITIGAAAGITGAGAGCAGCATGITITGCCCCACTGAAACTCCATCCTGCTGCCAGTG 120 300 360 360 420 9 TTCAAGATAGACTGGACTCTGTCACCAGGAGAGCACGCCAAGGACGAATATGTGCTATAC 1 ceecriceAsticcAstractes and a second contractic contr TIGGATITIGAAAGIIGAGAGCAGCAIGIITIGCCCCACIGAAACICAICCIGCIGCCAGIG TTACTGGATTATTCCTTGGGCCTGAATGACTTGAATGTTTCCCCGCCTGAGCTAACAGTC CATGTGGGTGATTCAGCTCTGATGGGATGTTTTTCCAGAGGCACAGAAGACAAATGTATA GACATCTTATGCAATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGA TTACTGGATTATTCCTTGGGCCTGAATGACTTGAATGTTTCCCCGGCCTGAGCTAACAGTC CATGTGGGTGATTCAGCTCTGATGGGATGTTTTTCCAGAGGCACAGAAGACAAATGTATA TATTACTCCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGCGTACACTTGATGGGG 61 241 241 301 61 121 181 181 301 361 셤 ò d δ g ò g à Ωp g ò ò

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421 ACCTATATCTGTGAAATCCGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTA 480

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(GETH) GENENTECH INC.

Godowski PJ; Paoni NF; Wood WI; Eaton Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, MA, Zhang

2003-288106/28 P-PSDB; ABU60611. New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, chromosome markers, or in generating probes.

Claim 2; Fig 303; 650pp; English

The invention discloses isolated PRO secreted/transmembrane polypeptides comprising a sequence without signal peptide and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that

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molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. The PRO polypeptides or polymocleotides are also useful in gene therapy, in chromosome identification, as chromosome markers, or in generating probes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and the isolated nucleic acids may be used for recombinantly expressing those markers. The PRO polypeptides and nucleic acids may also be used in tissue typing. Anti-PRO antibodies are useful in diagnostic assays for PRO, and in affinity purification of PRO from recombinant cell culture or matural sources. The sequences presented in ABX90083-ABX90468 are the genes encoding, the primers amplifying and the probes detecting the PRO polymucleotides of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at ó 240 240 120 120 180 180 300 300 360 360 420 420 480 480 540 540 600 600 960 720 9 9 TIGGATITIGAAAGITIGAGAGCAGCATGITITIGCCCACTGAAACTCATCCTGCTGCCAGTG CATGTGGGTGATTCAGCTCTGATGGGTGTTTTCCAGAGCACAGAGACAATGTATA TTCAAGATAGACTGGACTCTGTCACCAGGAGGAGGACGCCAAGGACGAATATGTGCTATAC 1 CGGCTCGAGTGCAGCTGTGGGGAGATTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATC CGGCTCGAGTGCAGCTGTGGGGAGATTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATC 61 TrgGartrrGaaaGrrGaaGcarGrrTrrGCCCACrGaaaCrCcarccrGcrGCCAGrG TTACTGGATTATTCCTTGGGCCTGAATGACTTGAATGTTTCCCCGCCTGAGCTAACAGTC TTACTGGATTATTCCTTGGGCCTGAATGACTTGAATGTTTCCCCGCCTGAGCTAACAGTC CATGTGGGTGATTCAGCTCTGATGGGATGTGTTTTCCAGAGGCACAGAAGACAAATGTATA TATTACTCCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGCGTACACTTGATGGGG GACATCTTATGCAATGATGGCTCTCTCTCTCTCCAAGATGTGCAAGAGGCTGACCAGGG ACCTATATCTGTGAAATCCGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGTA TTCCGCAATGACGGTTCCATCATGCTTCAAGGAGTGAGGGGGGTCAGATGGAGGGAAACTAC GACATCTTATGCAATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGA ACCTATATCTGTGAAATCCGCCTCAAAGGGGGAGGCCAGGTGTTCAAGAAGGCGGTGGTA crecardrecorrecadadececadadececenterecorrecades createres TCAGGACGCCGCAAAGGAGGAGTTGTATTCGTTACTACCACAAACTCAGGATGTCT GTGGAGTACTCCCCAGAGCTGGGGCCACTTCCAGAATCGTGTGAACCTGGTGGGGGCACATT ATGGGATGTGTTTTCCAGAGCACAGAAGTGAAACACGTGACCAAGGTAGAATGGATATTT ATGGGATGTGTTTTCCAGAGCACAGAAGTGAAACACGTGACCAAGGTAGAATGGATATTT TCAGGACGCCGCCAAAGGAGGAGATTGTATTTCGTTACTACCACAAACTCAGGATGTCT GTGGAGTACTCCCAGAGCTGGGGCCACTTCCAGAATCGTGTGAACCTGGTGGGGGGACATT TTCCGCAATGACGGTTCCATCATGCTTCAAGGAGTGAGGGAGTCAGATGGAGGAAACTAC for linking a bicactive .. DB 7; Length 1630; Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other; Indels 0; 100.0%; Score 1630; 100.0%; Pred. No. 0; cive 0; Mismatches specifically bind to the PRO polypeptide, seqdata.uspto.gov/sequence.html Best Local Similarity 100.0%; Matches 1630; Conservative (61 241 121 181 181 241 301 301 361 361 421 481 Query Match 421 481 541 541 601 601 661 661 721 유 임 ઠ ò à g ò g à 셤 δ 엄 ò 엄 ò g ò d ò ρp ठे 유 ò 셤

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The present invention relates to the isolation of novel human PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides and polymucleotides are useful for preparing a medicament useful in the diagnosis and treatment of tumours. Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting its expression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. Ack66841-ACA66962 represent cDNA sequences encoding the human PRO polypeptides of the invention. Note: The sequence data for this patent was obtained in sequence content of the sequence data for this patent was obtained in sequence uspective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TICAAGAIAGACIGGACICIGICACCAGGAGCACGCCAAGGACGAAIAIGIGCIAIAC 300
anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGGATITGAAAGITGAGAGCAGCATGITTTGCCCACTGAAACTCATCCTGCTGCCAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                             One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for the manufacture of a medicament for diagnosing or treating
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Smith V, Stephan JF, Watanabe CK,
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iive 0; Mismatches
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01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
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Matches 1630; Conservative
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Grimaldi JC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New genes, and its encoded secreted and transmembrane polypeptides, useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or pericyte proliferation, especially for treating lung tumors, arthritis
                                                                                          ACACTGGCCCTGGGAACCAGGCTGAGCTGAGTGGCCTCAAACCCCCCCGTTGGATCAGACC
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Smith V, Stephan JF,
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                GACATCTTATGCAATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGA
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lung tumour;

or

Wood WI;

PJ;

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cells, for stimulating proliferation of pericyte cells, or for modulating normal human dermal fibroblast proliferation. The PRO nucleic acid or polypeptide is also useful for treating tumours or various bone and/or cartilage disorders (e.g. sports injuries or arthritis), or wounds. The PRO polypeptides are useful in drug screening, particularly as targets for therapeutic intervention in these diseases, and in the diagnostic determination of the presence of these diseases, and in the diagnostic also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. This sequence encodes a novel human secreted and transmembrane PRO
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Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other;

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ογ	1 CGGC	CGGCTCGAGTGCAGCTGTGGGGAGATTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATC 60
qq	1 CGGC	GGGCTCGAGTGCAGCTGTGGGGAGATTCAGTGCATTGCCTCCCCTGGGTGCTTTCATC 60
٥,	61 TTGC	TIGGATTIGAAAGTIGAGAGCAGCATGTITIGCCCACTGAAACTCATCCTGCTGCCAGTG 120
Ср	61 TTGC	TIGGATITGAAAGITGAGAGCAGCAIGTITTGCCCACTGAACTCATCCTGCTGCCAGTG 120
δλ	121 TTAC	TTACTGGATTATTCCTTGGGCCTGAATGACTTGAATGTTTCCCCGCCTGAGCTAACAGTC 180
qo	121 TTAC	THE THE FIRST TRANSPORTED AND THE FIRST TRANSPORT TO THE
δ	181 CATC	CATGTGGGTGATTCAGCTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATA 240
Db	181 CATC	CAIGTGGGTGATTCAGCTCTGATGGGATGTGTTTTCCAGAGCACAAAAAAAA
ζ	241 TTC	TTCAAGATAGACTGGACTCTGTCACCAGGAGGACGCCAAGGACGAATATGTGCTATAC 300
Db	241 TTC	TICAAGATAGACTGGGACTCTGTCACCAGGAGAGCACGCCAAGGACGAATATGTGCTATAC 300
ò	301 TAT	TATTACTCCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGGGTACACTTGATGGGG 360
Db	301 TAT	TATTACTCCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGCGTACACTTGATGGGG 360
0y	361 GACZ	GACATCTTATGCAATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGA 420
QQ	361 GAC	GACATCTTATGCAATGATGGCTCTCTCTCTCTCAAGATGTGCAAGAGGCTGACCAGGGA 420
٥٨	421 ACC	ACCTATATCTGTGAAATCCGCCTCAAAGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTA 480
QQ	421 ACC	TATATCTGTGAAATCCGCCTCAAAGGGGGGGGGCGGTGTTCAAGAAGGCGGTGGTA 480
. vo	481 CTG(CTGCATGTGCTTCCAGAGGAGCCCAAAGAGCTCCATGGTGGGTG
Db	481 CTG	CTGCATGTGCTTCCAGAGGAGCCCAAAGAGCTCATGGTCCATGTGGGTGG
٥٨	541 ATG	ATGGGATGTGTTTTCCAGAGCACAGAAGTGAAACACGTGACCAAGGTAGAATGGATATTT 600
Db	541 ATG	ATGGGATGTGTTTTCCAGAGCACAGAAGTGAAAAAGTGTCAAGGTAGAATGGATTT 600
٥y	601 TCAC	TCAGGACGGCGCAAAGGAGGAGATTGTATTTCGTTACTACCACAAACTCAGGATGTCT 660
qa	601 TCAC	CAGGACGCCCCCAAAGGAGGAGATTGTTTCGTTACTACCACAAACTCAGGATGTCT 660
٥y	661 GTG	GTGGAGTACTCCCAGAGCTGGGGCCACTTCCAGAATCGTGTGAACCTGGTGGGGGACATT 720
Db	661 GTG	GTGGAGTACTCCCAGAGCTGGGGCCACTTCCAGAATCGTGAAACCTGGGGGGACATT 720
0y	721 TTC	TICCGCAATGACGGTTCCATCATGCTTCAAGGAGTGAGGAGTCAGATGGAGGAACTAC 780
Db	721 TTC	CGCAATGACGGTTCCATGTTCAAGGAGTGAGGGAGTCAGATGGAGGAAACTAC 780
δ	781 ACC	ACCTGCAGTATCCACCTAGGGAACCTGGTGTTCAAGAAACCATTGTGCTGCATGTCAGC 840

1140 1020 1080 1080 1260 1260 1320 1380 1380 1440 1500 1500 1020 CTCATIGITITICATACACTGAAGAIGGAGAATTIGGAGCCTGGCAGAGAGACTGGAC 1440 ACACTGGCCCTGGGAACCAGGCTGAGCTGAGTGGCCTCAAACCCCCCGTTGGATCAGACC 1560 CTCCTGTGGGCAGGCTCCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATAAAAACCAA 1620 CTCCTGTGGGGCAGGGTTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATAAAAACCAA 1620 AATCAGTTGGTGATCATTGTGGGAATTGTCTGTGCCACAATCCTGCTGCTCCCTGTTCTG AATCAGTTGGTGATCATTGTGGGAATTGTCTGTGCCACAATCCTGCTGCTCCTTTTTGT ATATTGATCGTGAAGAGCCTGTGGAAATAAGAGTTCAGTGAATTCTACAGTCTTGGTG GAAGGGGAGAACACATTTACTCCCCAATAATTGTACGGGAGGTGATCGAGGAAGAAGAA CCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCACCCAGTTTGGCCTTCTCTGAGG AGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGAGCATGGACTTGGCCTCTGGAGTGGG Adetrerogadesaacadecerdeerdadesaadesdadeacardeacererogaderes CCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGGCCTCTGGTCTTGGGTGT ccegaagagecregaacacregagececegecagecereagecereregecererege ATATTGATCGTGAAGAAGACCTGTGGAAATAAGAGTTCAGTGAATTCTACAGTCTTGGTG GAAGGGGAGAAACACATTTACTCCCCAATAATTGTACGGGAGGTGATCGAGGAAGAAGAA TCAGATCGGAACAACTCACTTGAAAAAAGTCAGGTGGGGGAATGCCAAAAACACAGCAA TGTGTCCTGGGCCACTCTACCAGTGATTTCAGACTCCCGCTCTCCCCAGCTGTCCTCGT CTCATTGTTTGGTCAATACACTGAAGATGGAGAATTTTGGAGCCTGGCAGAGAGACTGGAAC <u>AAGAACACGAAGAAGACTAATCCAGAGATAAAAGAAAAAACCCTGCCATTTTGAAAGATGT</u> TGTGTCCTGGGCCACTCTACCAGTGATTTCAGACTCCCGCTCTCCCCAGCTGTCCTCCTGT Human; PRO polypeptide; secreted protein; transmembrane protein; genetic disorder; antibacterial; immunosuppressive; transgenic; gene therapy; gene; ss. cDNA encoding human PRO1387 polypeptide. ABX64216 standard; cDNA; 1630 BP (first entry) CCCAAATCAA 1630 CCCAAATCAA 1630 26-FEB-2003 1021 1081 1141 1141 1261 1261 1321 1381 1441 1441 1501 1501 1561 1561 ABX64216; 841 901 196 1021 1081 1201 1321 1381 1621 1621 781 841 901 961 1201 RESULT 15 ABX64216 dd g g g 셤 셤 MAKAK BKAKAKA à g ò g 8 셤 ò 8 8 ò 8 g 8 ò δ ò ò 8 ò 8 g ਠੋ

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       Homo sapiens.
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25-FEB-1998;
20-MAR-1998;
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20-MAR-2000; 2
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15-MAY-2000; 2
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28-JUL-2000;
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GETH) GENENTECH LID

Godowski PJ; Paoni NF; Wood WI; Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL; Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, God Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paor Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Woc Zhang Z;

WPI; 2003-102117/09. P-PSDB; ABU13993.

Novel secreted and transmembrane polypeptide for modulating biological activity of cell expressing the polypeptide, identifying agonists or antagonists of polypeptide, and as molecular weight markers.

Claim 2; Fig 303; 649pp; English.

The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides, for including the bioactive molecules to calls expressing PRO polypeptides, for modulating biological activities of calls expressing PRO polypeptides, and for for identifying agonists or antagonists. The polymucleotide sequences cancing PRO polypeptides are useful as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for generating transgenic animals or knockout animals, to construct hybridisation probes for mapping the gene which encodes the PRO polypeptide, and for the genetic analysis of individuals with genetic disorders, in gene therapy, for chromosome condentification, as chromosome markers, and for sequence encodes a human PRO polypeptide of the invention. Note: The sequence catta for this patent was obtained in electronic format directly for the norms of the invention in the present the norms. from the USPIO web site at seqdata.uspto.gov/psipsDIDEntry.html

Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other;

0; Gaps DB 7; Length 1630; 0; Indels Query Match
100.0%; Score 1630;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1630; Conservative 0; Mismatches 0; Mismatches

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1081 GAAGGGAAACACATTTACTCCCCAATAATTGTACGGGAGGTGATCGAGGAAGAA 1140	Db 1321 TGTGTCTTGGGCCACTCTTCACAGTGATTTCAGACTCCCGCTCTCCAGTGTCTTCTCTTGTT 1380 Qy 1381 CTCATTGTTGGTCAATACACTGAAGATGGAGAATTTCGAGCCTGGCAGAGACTCTGGC 1440 Db 1381 CTCATTGTTTGGTCAATACACTGAAGATGGAGAATTTCGAGCCTGGCAGAGACTCGGA 1440 Qy 1441 AGCTCTGGAGAACAGCCTGCTGAGAGAGAGAATTTGGACTTGGCTTGCAGAGTGGA 1500	1441		Search completed: October 2, 2004, 00:28:37 Job time : 949 secs								
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1: /cgn2 6/ptodata/2/ina/5A COMB.seq:*

3: /cgn2 6/ptodata/2/ina/5B COMB.seq:*

3: /cgn2 6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2 6/ptodata/2/ina/6B COMB.seq:*

5: /cgn2 6/ptodata/2/ina/PCTUS COMB.seq:*

6: /cgn2 6/ptodata/2/ina/PcTUS COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-667-600A-144
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Patent No. 6602667

GENERAL INFORMATION:
APPLICANT: Walker, Michael G.
APPLICANT: Wolkmuth, Wayne
APPLICANT: Mindjer, Tod M.
TITLE OF INVENTION: Inflammation-Associated Polynucleotides
FILE REFERENCE: DB-0006-1 CIP
CURRENT FILING DATE: 2001-05-14

NUMBER OF SEQ ID NOS: 17

SEQ ID NO 11

LENGTH: 1751
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US-09-430-503-29
US-08-430-503-31
US-08-928-3838-1
US-09-272-496-1
US-09-376-496-1
US-09-134-001C-1793
US-08-134-001C-1793
US-08-134-002-3
US-08-416-478A-5
US-08-474-988B-5
US-08-394-442B-5
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1 US-08-073-799C-9
4 US-09-526-193A-22
4 US-09-976-594-136
4 US-08-997-685A-7
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4 US-09-446-301A-1
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 Best Local Similarity 99.9
Matches 1622, Conservative
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ORGANISM: Homo sapiens
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us-09-989-728-421.rni

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DB
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Pred. No. 0;
0; Mismatches
Patent No. 6444443
GENERAL INFORMATION:
APPLICANT: Gabor Jarai et al.
ITILE OF INVENTION: No. 6444443el Gene
FILE REFERRENCE: 4-31440Pl/NI/HO 29
CURRENT APPLICATION NUMBER: US/09/656,952
CURRENT FILING DATE: 2000-09-07
NUMBER OF SEQ ID NOS: 20
SEQ ID NO 17
                                                                                                                                                         Query Match
Best Local Similarity 97.6%;
Matches 1550; Conservative
                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                           ; ORGANISM: Hon
US-09-656-952-17
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                       AGGTAGAATGGATTTTTCAGGACGCCGCGAAAGGAGGAGATTGTATTTCGTTACTACC
                                                                        ACAAACTCAGGATGTCTGCGGAGTACTCCCAGAGCTGGGGCCACTTCCAGAATCGTGTA
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RESULT 3 US-09-656-952-17 ; Sequence 17, Application US/09656952

2 103 163 523 121 223 283 343 403 463 421 481 583 643 181 241 301 361 541 109 703 661 763 721 823 781 883 61 TCAGGAAGGCGGTGGTACTGCATGTGCTTCCAGAGGAGCCCAAAGAGCTCATGGTCCATG TCATCCTGCTGCCAGTGTTACTGGATTATTCCTTGGGCCTGAATGACTTGAATGTTTCCC TCATCCTGCTGCCAGTGTTACTGGATTATACCTTGGGCCTGAATGACTTGAATGTTTCCC CGCCTGAGCTAACAGTCCATGTGGGTGATTCAGCTCTGATGGGATGTGTTTTTCCAGAGCA CGCCTGAGCTAACAGTCCATGTGGGTGATTCAGCTCTGATGGGATGTGTTTTCCAGAGCA CAGAAGACAAATGTATATTCAAGATAGACTGGGACTCTGTCACCAGGAGAGCACGCCAAGG CAGAAGACAAATGTATATTCAAGATAGACTGGACTCTGTCACCAGGAGAGACACGCCAAGG 284 ACGAATATGTGCTATACTATTACTCCGAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACC ACGAATATGTGCTATACCTATTACTCCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACC GCGTACACTTGATGGGGGACATCTTATGCAATGATGGCTCTCTCCTGCTCCAAGATGTGC GCGTACACTTGATGGGGGACAACTTATGCAATGATGCCTCTCTCCTGCTCCAAGATGTGC AAGAGGCTGACCAGGGAACCTATATCTGTGAAATCCGCCTCAAAGGGGGGAGAGCCAGGTGT | TCAAGAAGGCGGTGGTACTGCATGTGCTTCCAGAGGGGGCCCAAAGAGCTCATGGTCCATG TGGGTGGATTGATTCAGATGGGATGTGTTTTCCAGAGCACAGAAGTGAAACACGTGACCA TGGGTGGATTCATTCAGATGGGATGTGTTTTCCAGAGCACAGAAGTGAAACACGTGACCA AGGTAGAATGGATATTTTCAGGACGCGCGCAAAGGAGGAGATTGTATTTCGTTACTACC ACAAACTCAGGATGTCTGTGGAGTACTCCCAGAGCTGGGGCCACTTCCAGAATCGTGTAA ACCTGGTGGGGGGACATTTTCCGCAATGACGGTTCCATCATGCTTCAAGGAGTGAGGGGT CAGATGGAGGAAACTACACCTGCAGTATCCACCTAGGGAACCTGGTGTTCAAGAAAACCA CAGATGGAGGAAACTACACCTGCAGTATCCACCTAGGGAACCTGGTGTTCAAGAAAACCA | TTGTGCTGCATGTCAGCCCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGGC ACCTGGTGGGGGACATTTTCCGCAATGACGGTTCCATCATGCTTCAAGGAGTGAGGGAGT Gaps 31; Length 1591 Indels 1; 4 ; 722 824

Query Match 91.0%; Score 1483.8; DB 4; Length 1592; Best Local Similarity 97.5%; Pred. No. 0; Matches 1550; Conservative 0; Mismatches 7; Indels 32; Gaps 3;	44 CCTGGGTGCTCTTCATCTTGGATTTGAAAGTTGAGAGCAGCATGTTTTGCCCACTGAAAC	Db 2 CCCTTGTGCTCTTCATCTTGGATTTGAAAGTTGAGGCAGGTGTTTTGCCCACTGAAAG 61 Qy 104 TCATCCTGCTGCCAGTGTTACTGGATTATTCCTTGGGCCTGAATGACTTGAATGTTTCC 163	Db 62 TCATCCTGCTGCCAGTGTTACTGGATTATACCTTGGGCCTGAATGATTGAATGTTTCCC 121 Qy 164 CGCCTGAGCTAACAGTCCATGTGGGTGATTCAGCTCTGATGGGATGTGTTTTCCAGAGCA 223		182 CAGAAGACAAATGTATATTCAAGATAGACTGGACTCTGTCACCAGGAGAGCAGGCCAAGG	284 ACGAATATGTGCTATACTATTACTCCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACC	Db 242 ACGAATATGTGCTATACTATTACTCCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACC 301 Qy 344 GCGTACACTTGATGGGGGACATCTTATGCAATGGTGTCTCTCTC	Db 302 GCGTACACTTGATGGGGGACAACTTATGCAATGGTGCTCTCTCCTCCTCCTCCTAGGTGC 361 Qy 404 AAGAGGCTGACCAGGGAACTTATGTGAAATCCGCCTCAAAGGGGAGAGCAGGTGT 463		OY 464 TCAAGAAGGGGTGGTTACTTGCATGCAGAGGAGCCCAAAGAGGTCCATGGTCCATG 523	524 TGGGTGGATTGATTCAGATGGGATGTGTTTCCAGAGCACAGAAGTGAAACAGGTGACCA	Db 482 TGGGTGGATTGATTCAGATGGGTGTTTTCCAGAGGAGGAGGAGGATGTATTTGGTTACTACC 543 Qy 584 AGGTAGAATGGATATTTTCAGGACGCGCGCAAAGGAGGAGATTGTATTTCGTTACTACC 643	Qy 644 ACAAACTCAGGATGTCTGTGGAGTACTCCCAGAGCTGGGGCCACTTCCAGAATCGTGTGA 703	704 ACCTGGTGGGGGACATTTCCGCAATGACGGTTCCATCATGCTTCAAGGAGTGAGGAGT	ON 764 CAGATGGAGGAAACTACACCTGCAGTACCACTAGGAACCTGGTGCTCAAGGAACTACAGGAACCTAGGGAACCTAGGGAACCTAGGGAACCTAGGAAACTACACTATCAAGGAACCTAGGAAACTACAACTATCAACTATCAAGGAACCTAGGAAACTAGAAAAACTAGAAAAACTAGAAAAAACTAGAAAAAACTAGAAAAAAAA	722 CAGATGGAGGAAACTACACCTGCAGTATCCACCTAGGGAACCTGGTGTTCAAGAAACCA	OY 824 TIGIGCTGCAFGTCAGCCCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGGC 883	Qy 884 CTCTGGTCTTGGGTAATCAGTTGGTGATCATTGTGGGAATTGTTGTGCCACAATCC 943	Qy 944 TGCTGCTCCTGTTCTGATATTGATCGTGAAGAGACCTGTGGAAATAAGAGTTCAGTGA 1003	04	962 AITCTACAGATCTTGGTGAAGAAGAGGAGGTAATCCAGAGATAAAGAAAAACC	Qy 1063 TGCCATTTTGAAAGATGTGAAGGGGAGAAA 1092
	842 CICIGGICIIGGGIGGIAAICAGIIGGIGAICAIIGIGGGAAIIGICIGIGCCACAAICC	QY 944 IGCTGCTCCCTGTTCTGATATTGATCGTGAAGACCTGTGGAAATAAGAGTTCAGTGA 1003	Qy 1004 ATTCTACAGTCTTGGTGAAGAACACGAAGAGACTAATCCAGAGATAAAAGAAAAACCCT 1063	Qy 1064 GCCATTTTGAAAGATGTGAAGGGAG	1094 ACATTACTCCCCATAATTACTCCCCCACAACAACAACAAC	1082 ACATITACICCCAATAATIGTACGGGAGGTGATCGAGGAAGAAGAACAAGTGAAAT 1	OY 1154 CAGAGGCCACCTACATGACCATTTGGCCTTCTCTGAGGTCAGATGGGAACA 1213	Qy 1214 ACTCACTTGAAAAAAAAGTCAGGTGGGGAATGCCAAAAACACAGCAAGCTTTTGAGAAG 1273 Db 1202 ACTCACTTGAAAAAAAGTCAGGTGGGGAATGCCAAAAACACAGCAAGCTTTTGAGAAG 1261	1274 AATGGAGAGTCCCTTCATCTCAGCAGCGGTGGAGACTCTCTCT	DD 1262 AATGGAGAGTCCCTTCATCTCAGGGGGGGGGGGACACTCTCTCT	1322 ACTCTACCAGTGATTTCAGACTCCCCGGCTGTCCTCCTCTGTTTTTTTT	QY 1394 CAATACACTGAAGATGGAGAATTTGGAGCCTGGCAGAGAGACTGGACGACTCTGGAGGAA 1453 Db 1382 CAATACACTGAAGATGGAGAATTTGGAGCCTGGCAGAGAACTGGACTGGACACAG-TCTGGAGGAA 1440	Db 1441 CAGGCCTGCTGAGGGAGGGAGCATGGACTTGGCCTCTGGAGTGGGACACTGGCCCTGG 1500 Qy 1514 GAACCAGGCTGAGTGACCTCCTCAAACCCCCCGTTGGATCAGACCCTCCTGTGAGCAG 1573	1501 GAACAGGCTGAGTGAGTGGCCTCAACCCCCCGTTGGATCAGGCCTCCTGTGTGTG	Db 1561 GGTTCTTAGTGGAAG 1588	RESULT 4	US-09-656-952-1 ; Sequence 1, Application US/09656952 ; Patent No. 6444443 ; CRNPRA. INFORMATION.	ø)	; CURRENT APPLICATION NUMBER: US/09/656,952; CURRENT FILING DATE: 2000-09-07; NUMBER OF SEQ. ID NOS: 20; SOFTWARE: PALENTIN Ver. 2.1	; SEQ ID NO 1 ; LENGTH: 1592 : TUBE: DNA	, ORGANISM: Homo sapiens US-09-656-952-1	

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                                                                     1454 CAGGCCTGCTGAGGGGAGGGAGCATGGACTTGGCCTCTGGAGTGGGACACTGGCCCTGG
                                                                                                                1334 ACTCTACCAGTGATTTCAGACTCCCGCTCTCCCAGCTGTCCTCCTGTCTCATTGTTTGGT
                                                                                                                                             901 ACTCTACCAGTGATTTCAGACTCCCGCTCTCCCAGCTGTCCTCTGTCTCATTGTTTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES TITLE OF INVENTION: ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,680 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive CITY: Cambridge STATE: MA STATE: MA ZIP: 0.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Springer, Suzanne A.
REGISTRATION NUMBER: P-41,323
TELECOMMUNICATION INFORMATION:
TELEPAK: (617) 498-8284
TELEFAK: (617) 496-8284
IELEFAK: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Jacobs, Kenneth
APPLICANT: MCGOY, John M.
APPLICANT: Racie, Lisa A.
APPLICANT: LaVallie, Edward R.
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Frans, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08867680
Patent No. 5958726
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Length 1024;
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APPLICANT: Dunas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: EXTRUDED CDNAS FOR SECRETED PROTEINS
FILE REFERENCE: 31.053.CIP
CURRENT APPLICATION WUMBER: 105/09/663,600A
CURRENT APPLICATION NUMBER: 09/191,997
PRIOR FILING DATE: 1998-11-13
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: 60/066,677
PRIOR PILING DATE: 1997-12-17
PRIOR PILING DATE: 1997-12-17
PRIOR PILING DATE: 1998-02-09
PRIOR PILING DATE: 1998-02-09
PRIOR PILING DATE: 1998-04-13
PRIOR PILING DATE: 1998-04-13
PRIOR PILING DATE: 1998-04-13
                                                   Indels
                                                                                                         7 GAGTGCAGCTGTGGGGAGATTTCAGTGCATTGCCTCCCCTGGGTGCT
Score 609.8; DB 2;
Pred. No. 1.3e-194;
                                                   0; Mismatches
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Query Match
Best Local Similarity 99.7°
Matches 611; Conservative
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; OTHER INFORMATION: n=a, g, c or US-09-663-600A-144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA CREATURE: CORGANISM: Homo sapiens FEATURE: Dolya signal LOCATION: 1113.-1138 NAME/KEY: POLYA site LOCATION: 1146.-1158 NAME/KEY: Misc_feature
                                                                                                     GENERAL INFORMATION:
                                                      US-09-663-600A-144
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Pred. No. 9.4e-153;
3; Mismatches 2; Indels 1;
                                                                                                                                        PARTURE:
NAME/KEY: sig_peptide
LOCATION: 214-339
OTHER INPORMATION: Von Heijne matrix
OTHER INPORMATION: Score 6.0999990463257
OTHER INPORMATION: Seq AlliloSQCAYWA/LP
NAME/KEY: PollyA signal
LOCATION: 1133.-1138
NAME/KEY: pollyA-site
LOCATION: 1146.-1158
NAME/KEY: misc_feature
LOCATION: 0146.-158
NAME/KEY: misc_feature
LOCATION: 0146.-158
OTHER INPORMATION: d: H64717
OTHER INPORMATION: d: H64717
OTHER INPORMATION: d: H64717
OTHER INPORMATION: d: H64717
OTHER INPORMATION: d: H65208
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OTHER INPORMATION: d: H65208
OTHER INPORMATION: d: H65208
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/099,273
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 229
SOFTWARE: Patent.pm
SEQ ID NO S0
LENGTH: 1158
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LOCATION: 652
SOTHER INFORMATION: n=a, g, c or
15.09-663-600A-50
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98.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 98.84
Matches 496; Conservative
                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                    APPLICANT: DUGGETT, ANGRETIC
APPLICANT: DUGGETT, ANGRETIC
APPLICANT: DUGGETT, ANGRETIC
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
FILE REFERENCE: 31.U83.CIP
CURRENT PILIOS DATE: 2000-09-15
PRIOR PAPLICATION NUMBER: 09/191,997
PRIOR PAPLICATION NUMBER: 00/191,997
PRIOR PAPLICATION NUMBER: 60/066,677
PRIOR APPLICATION NUMBER: 60/069,957
PRIOR APPLICATION NUMBER: 60/069,957
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1998-04-09
PRIOR PILING DATE: 1998-04-09
PRIOR PILING DATE: 1998-04-13
PRIOR PILING DATE: 1998-06-04
NUMBER OF SEQ ID NOS: 229
SECTION NUMBER: 60/099,273
PRIOR PILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 229
SEQ ID NO 144
                                                                                                      APPLICANT: Dumas Milne Edwards, Jean-Baptiste
Sequence 144, Application US/09663600A
Patent No. 6573068
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1152 ATCAGAGGCCACCTACATGACCATGCACCAGTTTGGCCTTCTCTGAGGTCAGATCGGAA 1211
                                                                                                    1092 ACACATTTACTCCCCAATAATTGTACGGGAGGTGATCGAGGAAGAAGAACCAAGTGAAAA 1151
                                                                                                                                                          1212 CAACTCACTTGAAAAAGTCAGGTGGGGGAATGCCAAAAACACAGCAAGCCTTTTGAGA 1271
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                                                                                                                                                                                730 GACGGTTCCATCATGCTTCAAGGAGTGAGGGAGTCAGATGGAGGAAACTACACCTGCAGT
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TITLE OF INVENTION: COMPOSITIONS AND METHO
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANC
FILE REPERENCE: 210121.478C14
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILIG DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
SOFTWARE: PASTSEQ for Windows Version 3.0
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Sequence 1549, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
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Bangur, Chaitanya S.
Lodes, Michael A.
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Bangur, Chaitanya
Lodes, Michael A.
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Vedvick, Tom
Carter, Darrick
Retter, Marc
Mannion, Jane
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Vedvick, Tom
Carter, Darrick
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Matches 91; Conserv
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                                                                                                                                                                                                                                                                                                                                        RESULT 10
US-09-702-705-1549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1032 GAAGACTAATCCAGAGATAAAAGAAAACCCTGCCATTTTGAAAGATGTGAAGGGGGAGAA 1091
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  427 ATCTGTGAAATCCGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCAT
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3.2%; Score 51.6; DB 1; Length 7218;
Best Local Similarity 6.8%; Pred. No. 5.6e-06;
Matches 24; Conservative 188; Mismatches 142; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: VA
CUUNTER: VA
ZIP: 22313-0299
COMPUTER READBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OFBRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE: CLASSIFICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE: 26.406.1991
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26.406.1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 30472/114 IMMU
TELEBENONE: (703)85.3300
                                                                                                                                                                                                                                                      US-08-212-463-14/C
Sequence 14, Application US/08232463
Fatent No. 5670367
FAPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLFOX VIRUS
NUMBER OF SEQUENCES: 5.2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
                                                                                                                                           487 GTGCTTCCAGAGGAGCCCAAAG 508
                                                                                                                                                                              494 GTGCTTCCAGAGGAGCCCAAAG 515
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TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
...MTH: 7218 base pairs
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TYPE: nucleic acid
STRANDEDNESS: single
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New Proteins Produced By Human
Lymphocytes, DNA Sequences Encoding These Proteins And
Their Pharmaceutical And Biological Uses
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           262 CCCAAAICCTTTGGGTCACCTGGAICCCTGGGGAAGCTGCTTTGTGAGGTGACTC 316
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Pred. No. 0.0035;
0; Mismatches 84; Indels
                                                                                                                                                                                                                                                               APPLICANT: Vedvick, Tom
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Carter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
ITILE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C12
CURRENT APPLICATION NUMBER: US/09/671,325
CURRENT FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 1825
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPALIANT COMPUTER: IBM PC COMPUTER: DESTATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATH: US/08/416,478A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEE: BROWDY AND NEIMARK, P.L.L.C.
: 419 Seventh Street, N.W., Suite 400
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 1, Application US/08416478A; Patent No. 5773578
; GENERAL INFORMATION:
APPLICANT: Hercend, Thierry
APPLICANT: Triebel, Frederic
TITLE OF INVENTION: Lymphocytes, DN:
TITLE OF INVENTION: Lymphocytes, DN:
TITLE OF INVENTION: Their Pharmaceu
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                   Sequence 1549, Application US/09671325
Patent No. 6667154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.5%;
                                                                                                                                                                                Wang, Tongtong
Bangur, Chaitanya
Lodes, Michael A.
                                                                                                                                                                                                                                                    Fanger, Gary
Vedvick, Tom
Carter, Darrick
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 91; Conserv
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                                                                                                                                                              GENERAL INFORMATION:
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STATE: D.C
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US-08-416-478A-1
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APPLICANT:
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APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILLING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SSOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 438
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Pred. No. 0.0035;
0; Mismatches 84; Indels
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C9
CURRENT APPLICATION NUMBER: US/09/614,124B
CURRENT FILING DATE: 2001-07-11
SUMMER OF SEQ ID NOS: 1668
SOFTWARE: FASTESEQ for Windows Version 3.0
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Pred. No. 0.0035;
0; Mismatches 84;
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; Sequence 1549, Application US/09614124B
; Patent No. 6630574
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52.0%; Pred
0;
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APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
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Vedvick, Tom
Carter, Darrick
Retter, Marc
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Best Local Similarity 52.0°
Matches 91; Conservative
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US-09-736-457-1549
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Best Local Similarity
Matches 91; Conserv
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APPLICANT:
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APPLICANT:
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ATTORNEY/AGENT INFORMATION:
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EDNESS: single
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231..1724
                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                     TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: line
                                                                                                                                                                                                                                                                                                    , NAME/KEY:
, LOCATION:
US-08-474-988B-1
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Job time
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LYMPHOCYTES, DNA SEQUENCES ENCODING THESE PROTEINS AND
THEIR PHARMACEUTICAL AND BIOLOGICAL USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1173 GACTTTACCCTTCGACTAGAGGATGTGAGCCAGGCCCAGGCTGGGACCTACACCTGCCAT 1232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          790 ATCCACCTAGGGAACCTGGTGTTCAAGAAACCATTGTGCTGCATGTCAGCCCGGAAGAG 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  730 GACGGTTCCATCATGCTTCAAGGAGTGAGGGAGTCAGATGGAGGAAACTACACCTGCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.5%; Score 40.6; DB 1; Length 1871; 52.0%; Pred. No. 0.01; cive 0; Mismatches 84; Indels 0
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,988B
FILING DATE: 0-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/416,478
FILING DATE: 04-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/854,644
FILING DATE: 08-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hercend, Thierry
APPLICANT: Triebel, Frederic
TITLE OF INVENTION: LYMPHOCYTES, DNA SEQUENCES I
TITLE OF INVENTION: THEIR PHARMACEUTICAL AND BIC
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: US 07/854,644
FILING DATE: 08-5EP-1992
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REPERBNENCE/DOCKET NUMBER: HERCEND=1A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1871 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 52.0%
Matches 91, Conservative
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COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                              CDS
231..1724
                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY:
; LOCATION:
US-08-416-478A-1
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US-08-474-988B-1
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| REGISTRATION NUMBER: 37,971 | REGISTRATION NUMBER: 18791 | REGISTRATION NUMBER: 1870 | RECOMMUTATION INFORMATION: | TELEPROXED | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870 | 1870
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

Run on:	Octo	October 1, 2004, 19:38:55; Search time 10107 Seconds
		(Without alignments) 6990.120 Million cell updates/sec
Title: Perfect score: Sequence:	US-09 1630 1 cgc	US-09-989-728-421 1630 1 cggctcgagtgcagctgtggtaaaaaccaaccaaatcaa 1630
Scoring table:	IDENTI Gapop	IDENTITY NUC Gapop 10.0 , Gapext 1.0
Searched:	347	3470272 seqs, 21671516995 residues
Total number of	hits	satisfying chosen parameters: 6940544
Minimum DB seq Maximum DB seq	length: length:	h: 0 h: 2000000000
Post-processing		Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database :	G G G G G G G G G G G G G G G G G G G	: * :: * :: * :: * :: * :: * :: * :: *
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. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	AR252655	AX358942	AX362435	AX403534	AA454648	AX464386 AX491126	AY358362	BD248693	AR373044 Segue	AY138965	AR225785 Seque	AX347902 RD200075	AX833028	AK094399	AR225784	AX347901 A.TS15553	AR225769	AX347885	AX083427 AB379586	AX834666		BD139315 AK090409	AR075998	AX714902 Sequence	AK057590 Homo		BD006702 Novel	AR340723 Seque	AR340770 Sequence	BD085902 Elongati		BC050133 Mus		AC068591 Homo	BD139373 Exter	BD058271 Secre	0 10 10 10 10 10 10 10 10 10 10 10 10 10		0 bp DNA linear DAT 20_DEC_2002	5478825.				ove M. T. And		
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Catarrhini; Hominidae; Homo.
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   ATATTGATCGTGAAGAGCCTGTGGAAATAAGAGTTCAGTGAATTCTACAGTCTTGGTG
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Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V.,
Watanabe,C.K. and Wood,W.I.
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Mammalia; Eutheria; Primates;
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Secreted and transmembrane polypeptides and nucleic acids encoding
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                                                                    GAAGGGGAGAAACACATTACTCCCCAATAATTGTACGGGAGGTGATCGAGGAAGAAGAACA
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                                         1021 AAGAACACGAAGAAGACTAATCCAGAGATAAAAGAAAAAACCCTGCCATTTTGAAAGATGT
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Sequence 195 from Patent W00208288.
AX362435
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Dest Local Similarity 100.0%; Scote 1630; DB 6; Length 1630; Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 0; Indels 0; Gaps 0; Conservative 0;	

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Euthería, Primates, Catarrhini, Hominidae, Homo.
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Genentech Inc. (US)
Location/Qualifiers

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Query Match 100.0%; Score 1630; DB 6; Length 1630; Best Local Similarity 100.0%; Pred. No. 0; 0; Indels 0; Gaps 0; QY 1 CGGCTCGAGTGCAGCTGTGGGAGATTTCAGTGCTTCCCCTGGGTGCTCTTCATC 60 Db 1 CGGCTCGAGTGCAGCTGTGGGAGATTTCAGTGCTCCCCTGGGTGTTCTTCATC 60 Db 1 CGGCTCGAGTGCAGCAGCAGATTTTGCCCACTGAAACTCATCCTGCTGCCAGTG 120 Qy 61 TTGGATTTGAAAGTTAGAAGCAGCATGTTTTGCCCACTGAAACTCATCCTGCTGCCAGTG 120 Db 61 TTGGATTTGAAAGTTTTTGCCCACTGAAACTCATCACACTGAAACTCATCACACTGAAACTCATCACACTGAAACTCATCACACTGAAACTCATCACACTGAAACTCATCACACTGAAACTCATCACACTGAAACTCATCACACTGAAACTCATCACAAACTACACAACACAGCAACTGAAAACTCATCACAAACTACACACTGAAAACTCATCACAAACTACAAACTACAAACTACAAACTACAAAACTACAAACTACAAAAACTACAAAAACTACAAAAAA	AGCTAACAGTC 18 AGCTAACAGTC 18 AGCTAACAGTC 18 ACAAATGTATA 24	TTCAAGATAGACTGGACTCTGTCACGAGAGGCCAAGGACAAGACAATATA TTCAAGATAGACTGGACTCTGTCACCAGGAGAGCCCAAGGACGAATATGTGCTATAC TTCAAGATAGACTGGACTCTGTCACCAGGAGAGCACGCCAAGGACGAATATGTGCTATAC TATTACTCCAATCTCAGTGCCTATTGGGCGCTTCCAGAACGGCACACCACTTGATGGGG	GACATCTTATGCAATGGCTCTCTCGCTCCAGATGTGCAAGAGGGTGACCAGATGTATTATGCAATGATGGCTGCTCCTCCTCCAAGATGTGCAAGAGGGTGACCAGACAGA	481 ALGGARGEGETECAGAGAGAGAGAGAGAGAGAGAGAGAGAGGAGAG			841 CCGGAAGACCTCGAACACTGGTGACCCCGGCAGCCCTGAGGCCTCTGGTCTTGGGTGGT 900	901 AATCAGTIGGIGATCATTGIGGGAATTGICIGIGCCACAATCCTGCTGCTCCCTGTTCTG 960 961 ATATIGATCGIGAAGAAGACCTGGGAAATAAGAGTICAGTGAATTCTACAGTCTTGGIG 1020	5

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Best Local Similarity 100.0%; Pred. No. 0; Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 CGGCTCGAGTGCAGCTGTGGGAGATTTCAGTGCATTGCCTCCCTGGGTGCTCTTCATC 60 Db 1 CGGCTCGAGTGGGGAGATTTCAGTGCATTGCCTCCCTGGGTGCTTTCATC 60 Qy 61 TTGGATTTGAAAGTTGAGAGCAGCATGTTTTGCCCACTGAACTCATCCTGCTGCGGTG 120 Db 61 TTGGATTTGAAAGTTGAGAGCAGCATGTTTTGCCCACTGAAACTCATCCTGCTGCCAGTG 120	121 121 121	241 TTCAAGATAGACTCTGTCACCAGAGAGAGCACGCCAAGACGAATATGTCTATAC 241 TTCAAGATAGACTGTCACCAGGAGAGAGCACGCCAAGGACGAATATGTCTATAC 241 TTCAAGATAGACTCTGTCACCAGGAGAGCACGCCAAGGACGAATATGTCTATAC 301 TATTACTCCAATCTCAGTGTCCTATTGGGCGCTTCCAGAACCGCGTACACTTGATGGGG	Db 301 TATTACTCCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGCGTACACTTGGGGGG 380 94 361 GACATCTTATGCAATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGA 420 Db 361 GACATCTTATGCAATGGCTCTCTCCTGCTCCAAGAGTGCCAAGAGGCTGACCAGGGA 420	421 ACCTATATCTGTGAAATCCGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTA 421 ACCTATATCTGTGAAATCCGCCTCAAAGGGAGAGACCAGGTGTTCAAGAAGGCGTGGTA	QY 481 CTGCATGTGCTTCCAGAGGCCCAAGAGCTCATGGGTCGATTGG5 540	Db 541 ATGGGATGTTTTCCAGAGCACAGAAGTGAAACACGTGACCAAGGTAGAATGGATATTT 600 Qy 601 TCAGGACGGCGCAAAGGAGAATGTATTTTTCGTTACTACCACAAACTCAGGATGTCT 660 Db 601 TCAGGACGGCGCGCAAAGGAGGATTGTATTTCGTTACTACCACAAACTCAGGATGTCT 660	661 GTGGAGTACTCCCAGAGCTGGGGCCACTTCCAGAATCGTGTGA	CUCCAA GALGA LUCAT LATECT CAAGAA GAAGAA GAAGAA GAAGAA GAAGAA CAAGAA GAAGAA GAAGAA GAAGAA GAAGAA GAAGAA	CCTGCAGTATCCACCTAGGGAACCTGGTGTTCAAGAAAACCATTGTGCTGCATG CGGAAGAGCCTCGAACCTGGTGTTCAAGAAAACCATTGTGCTGCTG CGGAAGAGCCTCGAACACCTGGTGACCCCGGCAGCCCTGAGGCTCTCGGTCTTGG CGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGGCCTCTGGTCTTGG	OY 901 AATCAGTTGGTGATCATTGTGGGAATTGTCTGTGCCACAATCCTGCTGCTCCTGTTCTG 960	Qy 961 ATATTGATGGTGAAGAAGACCTGTGGAAATAAGAGTTCAGTGAATTCTACAGTCTTGGTG 1020 	OY 1021 AAGAACACGAAGAACTAATCCAGAGATAAAAGAAAAACCCTGCCATTTTGAAAGATGT 1080

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                                                                                       Homo sapiens (numan)
Homo sapiens (numan)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 1751)
Malaila; Buthoria; Primates; Catarrhini; Hominidae; Homo.

Inclammation-associated genes
Inflammation-associated genes
Atent: JP 2002530077-A 11 17-SEP-2002;
INCYTE PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002530077-A/11
PD 17-SEP-2002
PR 18-NOV-1999 JP 2000582557
PR 18-NOV-1999 JP 200058257
PR 18-NOV-1999 JP 2000582557
PR 18-NOV-1999 JP 20058257
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
       Inflammation-associated
                     BD248693.1 GI:33058463
JP 2002530077-A/11.
                                                                             Homo sapiens (human)
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Inflammation-associated polynucleotides
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/organism="unknown"
/mol_type="genomic DNA"
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IMLQQVRESDGGNYTCSILLGNLVFKKTIVLHVSPEBFRLVTPAALARPLVLGGNQLV
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Catarrhini; Hominidae; Homo
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Foster, J.S. and Gurney, A.L.
Direct Submission
Submitted (02-AUG-2002) Molecular Biology, Genentech, 1
South San Francisco, CA 94080, USA
Location/Qualifiers
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protein id="AAN52117.1"
db_xref="G1:27762122"
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_txref="taxon:9606"
1. 1635
/gene="AMICA"
76. .1260
AV138965
Homo sapiens adhesion molecule A
AV138965
                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                   GI:27762121
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                                                                                                                                                                                                                                                                                                                    gene="AMICA"
                                                                             Homo sapiens (human)
                                                                                            Homo sapiens
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Best Local Similarity
Matches 1621; Conserv
                                                 AY138965.1
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570 GCAGG 561 GCAGG 630 A 163	RESULT 12	Gaps Gaaac 10 Gaaac 11 Gaaac 61 TTCCC 16 Gagca 22 Gagca 18 Gagca 23 Gagca 24 Caagca 24 Caagca 24 Caagca 24 Caagca 16 Caagca 24 Caagca 24 Caagca 26 Ca	v 4 7 7 7

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 1649)

E Hillman, J.L., Bandman, O., Lal, P., Yue, H., Reddy, R., Tang, T.Y.,

Gerstin, E.H., Patterson, C., Baughn, M.R., Azimzai, Y. and Lu, D.A.M.

Human transcriptional regulator molecules

I NCYTE PHARMACEUTICALS INC

OS Homo sapiens (human)

PN JP 2002513554-A,47

DD 14-MAY-2002

PF 04-MAY-1999 US 60/084254,07-AUG-1998 US 60/095827 PR
02-OCT-1998 US 60/102745
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                              CTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGGAATTGTCTGTGCCACAATCC
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1 Human transcriptional regulator mo
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JP 2002513554-A/47.

Homo sapiens (human)
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             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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                                                         Jarai, G. and Yousefi, S.

Novel gene
Patent: WO 0187938-A 18 22-NOV-2001;
Location/Qualifiers
1. 1561
/ Organism="Homo sapiens"
/ Organism="Homo sapiens"
/ Ab_xref="taxon:9606"
                                                                                                                                                                                                                           ; Score 1534.8;
; Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.5%;
Matches 1550; Conservative
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                 819 ATTGTGCTGCATGTCAGCCCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGG
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                                                                                                                       CIGCTGCTCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAAATAAGAGTTCAGTG
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     ATTGTGCTGCATGTCAGCCCGGAAGACCTCGAACACTGGTGACCCCGGCAGCCCTGAGG
                                                      CCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGGAATTGTCTGTGCCACAATC
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PC CI2N15/09,A61K38/00,A61K45/00,A61P35/00,A61P37/02,A61P43/00
PC CO7K14/47,
PC CO7K16/18,C12N1/15,C12N1/19,C12N1/21,C12NS/10,C12Q1/68//C12P21/
JENNIFER L HILLMAN, OLGA BANDMAN, PREETI LAL, HENRY YUE, ROOPA
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                                                                                                                                                                 /organism='Homo sapiens (human)'.
Location/Qualifiers
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Pred. No. 0;
0; Mismatches 12; Indels
                                                                                                              C12P21/08,C12N15/00,A61K37/02,C12N5/00
Incyte clone 319415CB1
Key Location/Qualifiers
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/organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
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Full-length cDNA sequences
Patent: EP 1347046-A 152 24-SEP-2003;
Research Association for Biotechnology
Location/Qualifiers
                                                                                                 Score 1499.8; pred. No. 0; 0; Mismatches
                                       1. .1959
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                  Similarity 99.9%; Conservative
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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ALIGNMENTS

AY420493 Pan troglodytes HCM7242 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.	AY420493.1 GI:39776450 GSS. Pan troglodytes (chimpanzee) Pan troglodytes Eukaryotes, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.	<pre>1 (bases 1 to 911) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.</pre>	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios Science 302 (5652), 1960-1963 (2003) 14671302	<pre>2 (bases 1 to 911) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. Direct Submission</pre>
AY420493 Pan trog genomic a	AY420493 GSS. Pan trog Pan trog Eukaryot Mammalia	1 (base Clark,A. Todd,M.A Ferriera Adams,M.	Inferring gene trios Science 30 14671302	2 (base Clark, A. Todd, M.A Ferriera Adams, M.
RESULT 1 AY420493 LOCUS DEFINITION ACCESSION	VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS	TITLE JOURNAL PUBMED	REFERENCE AUTHORS TITLE

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BX402821
BX402821 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED Homo sapiens CDNA clone CSODJ006YB01 3-PRIME, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 898)
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6071.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSIAJ002ZD01NP1&cluster=6071.r. Contact
Peng Liang Bmail: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Paraday Avenue Genoscope sequence ID: CSIAJ002ZD01NP1.
Location/Qualifiers
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                                                                                               1. 911
/organism="Pan troglodytes"
                                                                                                                             /mol_type="genomic_DNA"
/db_xref="taxon:9598"
                                                                                                                                                                                     /locus_tag="HCM7242"
                                                         based on alignment.
Location/Qualifiers
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778 839 838 779 898 719

Gaps

Docation/Qualifiers Location/Qualifiers Source 1. 1054	Query Match 51.5%; Score 838.8; DB 13; Length 1054; Best Local Similarity 92.5%; Pred. No. 1.8e-212; Matches 910; Conservative 13; Mismatches 55; Indels 6; Gaps 4;	Qy 21 GGAGATTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATCTTGAAAGTTGAGAG 80	OY 81 CAGCATGTTTTGCCCACTGAAACTCATCCTGCTGCCACTGTTACTGGATTATTCCTTGGG 140	QY 141 CCTGAATGACTTGAATGTTTCCCCGCCTGAGCTAACAGTCCATGTGGGTGATTCAGCTCT 200	Qy 201 GAIGGGAIGIGTITICCAGAGCACAGAAGACAAATGIAIATITCAAGAIAGACIGGACICT 260	OY 261 GTCACCAGGAGGACGCCAAGGACGAATATGTGCTATACTATTACTCCAATCTTAGTGT 320	Oy 321 GCCTATTGGGGCGCTTCCAGAACCGCGTACACTTGATGGGGACATCTTATGCAATGGTGG 380	0y 381 CTCTCTCTGGCTCCAAGAGGCTGACCAGGAACCTATATCTGGAATCCG 440 bb 429 CTCTCTCTGGTCTCCAAGAGGCTGACCAGGGAACCTATATCTGTGAATCCG 488 Cy 441 CTCTCAAGGGACGAGTGTTCAAGAGGCTGACCTGATATCTGTGAATCCG 488 Cy 441 CTCTCAAGGGACGCAGGTGTTCAAGAGGCTGGTACTGCATGTGTTTCCAGAGGA 548 Cy 489 CCTCAAGGGAGAGGCCAGGTGTTCAAGAGGCGGTGGTACTGCATGTGTTTCCAGAGGA 548 Cy 501 GCCCAAAGGGCAGGTCATGTGGGTGTTTCAAGATGGGATGTTTTCCAGAGGA 548 Cy 501 GCCCAAAGAGCTCATGTGGGTGGATTGATTCAGATGGATG
QY 959 TGATATTGATCGTGAAGACCTGTGGAAATAAGAGTTCTAGTGATTCTACAGTCTTGG 1018 Db 658 TGATATTGATCGTGAAGAACCTGTGGAAATAAGAGTTCAGTGAATTCTACAGTCTTGG 599 QY 1019 TGAAGAACACGAAGACTAATCCAGGATAAAAGAAAACCCTGCCATTTTGAAAGAT 1078 Db 598 TGAAGAACACACATTACTCCCCAATAATCTACGGCAGCTTTTGAAAGAT 539 QY 1079 TGAAGAACACACATTACTCCCCAATAATTGTACGGCAGTACATCGAAGAACGTTTTGAAAGAT 539 Db 538 GTGAAGGGGAAAACAATTAACTCCCCCAATAATTGTACGGGAAGAAG 479 QY 1139 AACCAGTGAAAAACAATTAACTCCCCCAATAATTGTACGGCACATCGAGGAAGAAG 479 QY 1139 AACCAGTGAAAAAACAATTAACTCCCCAATAATTGTACGCCCCCAGTTTGGCCTTCTCTGA 479 QY 1139 AACCAAGTGAAAAATCAGAGCCCCCCACTGCACTGCACCCCAGTTTGGCCTTCTCTGA 1198 AR AACCAAGTGAAAAATCAGAGCCCCCCATGCACTGCACCCCAGTTTGGCCTTCTTCTGA 1198	1199	Oy 1259 AAGCTTTTGAGAAGAAGGAGGTCCCTTCATCTCAGCAGGGGGGAGACTCTCCTG 1318 	Qy 1319 TGTGTGTCCTGGGCCACTCTACCAGTGATTTCAGACTCCCGCTCTCCCAGCTGTCCTCCT 1378	Qy 1379 GTCTCATTGTTTGGTCAATACACTGAAGATTTGGAGCCTGGCAGAGACTGG 1438	QY 1439 ACAGCTCTGGAAGAACAGGCCTGCTGAGGGAAGGAAGCATGGCCTTGGCCTCTGGAGTG 1498	OY 1499 GGACACTGGCCTGGCAACCAGGCTGAGCTGAGCCTCAAACCCCCGTTGGATCAGA 1558	OY 1559 CCCTCCTGTGGGGGGTTCTTAGTGGAGTTACTGGGAAGAATCAGAGATGA 1613	BESULT 3 BX346274 LOCUS BX346274 LOCUS BX346274 LOCUS BX346274 BX346

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AY420492 911 bp DNA linear GSS 12-DEC-2003
Homo sapiens HCM7242 gene, VIRTUAL TRANSCRIPT, partial sequence,
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Clark, A.G. Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Reritara, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, White, T.J., Sninsky, J.J., Inferring nonneutral evolution from human-chimp-mouse orthologous
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/tissue type="B CELLS (RAMOS CELL LINE)"
/tissue type="B CELLS (RAMOS CELL LINE)"
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/coll line="RAMOS CELL LINE"
/note="Vector: PCMVSPORT 6; 1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECRYV sites of the pCMVSPORT 6 vector. Library was not normalized."
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BX421455 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens cDNA clone CSODG006YD16 5-PRIME, mRNA sequence.

BX421455
BX421455.1 GI:30766084
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1 (bases 1 to 911)

1 'M.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization
Unpublished (2001)
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6071.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODG006DB08QPl&cluster=6071.r. Contact :
Feng Liang Email : fliang@alifetech.com URL :
http://fullength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODG006DB08QPl.
Location/Qualifiers
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Pred. No. 8.4e-212;
3; Mismatches 6; Indels 1;
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Db 721 CTGGTGTTCAAGAAACCATTGTGCTGCATGTCAGCCCGGAAGACCTCGAAC	RESULT 6 BA414034/c BA414034 LOCUS BX414034 DEFINITION BX414034 DEFINITION BX414034 HOMO SapienS B CELLS (RAMOS CELL LINE) Homo Sa	3-PRIME, mB 7423 Chordata	Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Hon REFERENCE 1 (bases 1 to 915) AUTHORS 11,WB., Gruber,C., Jessee,J. and Polayes,D. TITLE Full-length CDNA libraries and normalization JOURNAL Unpublished (2001) COMMENT Contact: Genoscope Genoscope - Centre National de Sequencage RP 191 9101 91016 EVEN CONTACT	Email: segret@genoscope.cns.fr, Web : www.genoscope.cns Library was constructed by Life Technologies, a division Invitrogen. This sequence belongs to sequence cluster 6(more information about this cluster, see http://www.genoscope.cns.fr/	Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ InVitroGen Corporation Faraday Avenue Genoscope sequence ID: CSOBAKO46ABIINM1 FEATURES Location/Qualifiers 1.915 /organism="Homo sapiens" /mol_type="mRNA"	/ db xref="taxon:9606" /clone="CSODGO06VBT6" / Lisue type="B CELLS (RAMOS CELL LINE)" / clone line="RAMOS CELL LINE" / clone line="to serve the line" (RAMOS CELL LINE)" / note="vector: pCWVSPORT 6; lat strand cDNA was with a Notl-oligo(dT) primer. Five prime end er	double-Strand cDNA was digested with Not I and the Not I and EcoRV sites of the pCMVSPORT 6 ve Library was not normalized."	Ouery Match 50.8%; Score 827.4; DB 13; Length 915; Best Local Similarity 96.7%; Pred. No. 1.9e-209; Matches 887; Conservative 0; Mismatches 26; Indels 4;	Oy 711 GGGGACATTTCCGCAATGACGGTTCCATCAT-GCTTCAAGGAGTGAGGGAGT Db 914 GGGGGACATTTAACGCAAAAACGGTGCCTCCTGGCTCCAAGAAGTGAGGGAGT	QY 770 GAGGAAACTACACCTGCAGTAICCACCTAGGGAACCTGGTGTTCAAGAAAACCA DD 854 GAGGAACTTACACCTGCAGGTTCCACCTAGGG-ACCTGGTGGTCAAAAAAACCA	Qy 830 IGCAIGTCAGCCCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCTGAGGC
2 (bases 1 tc Clark, A.G., G] Todd, M.A., Tar Pertrera, S., Adams, M.D. and Direct Submiss Submisted (16. Rockville, MD This sequence based on align	1>911 /locus_tag="HCM7242" 50.8%: Score 828 4. DB 29	i Indels ACTGGATTATT ACTGGATTATT ACTGGATTATT	Qy 145 AATGACTTGAATGTTTCCCCGCCTGAGCTAACAGTCCATGTGGGTGATTCAGCTCTGATG 204 Db 61 AATGACTTGAATGTTTCCCGGCCTGAGCTAACAGTCCATGTGGGTGATTCAGCTCTGATG 120 Qy 205 GGATGTGTTTTCCAGAGCAGAAGACAATGTATATTCAAGATGACTGGTCTGTCA 264 Db 121 GGATGTGTTTTCCAGAGCACAGAAGAATGTATATCAAAATAGTTCAAAATAGTCTCTCA 180	OY 265 CCAGGAGAGCACGCAAAGACGAAAATGAGTAATACTATTACTCCAATCTCCAATGTGCCT 324	TCTTATGCAATGATGGCTCT ATATCTGTGAAATCCGCCTC	361 AAAGGGAGAGCCAGGIGTTCAAGAAGGCGGTGGTACTGC 505 AAAGAGCTCATGGTGGTGGGTGGATTCAGTTCAGATGG 421 AAAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	565	625	685	745	Qy 805 CTGGTGTTCAAGAAAACCATTGTGCTGCATGTCAGCCCGGAAGAGCCTCGAACACTCGGG 864

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TGCAAGTCAGCCCGGAAGAGCCTCGAACACTGGTGGCCCCCGGCAGCCCTAAGGCCTCTGG
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. II (bases 1 to 1015)
MH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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/tau .uoctar. Univo.
/clone lib="NIH MGC 115"
/note="Organ: pooled brain, lung, testis; Vector:
/note="Organ: pooled brain, lung, testis; Vector:
powr-Sporfs; Site_1: Not!; Site_2: Escok' (destroyed); RNA powre anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dr primed and directionally cloned (Recok' site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb, Library is normalized and enriched for full-langth clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
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Tissue Procurement: Life Technologies, ......

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:

http://amage.llnl.gov

Plate: LLAM12789 row: j column: 24

High quality sequence stop: 699.

Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:5753591"
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/ (db_xref="taxon:9606"  
/ (clone="INMES:5226473"  
/ (clone="INMES:5226473"  
/ (clone lib="NHI MGC 120"  
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1 (bases 1 to 849)

S NIH-MGC http://mgc.nci.nih.gov/.

L National Institutes of Health, Mammalian Gene Collection (MGC) Ontpublished (1999)

L Ontpublished (1999)

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.

CONTACT: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be http://image.llnl.gov
Plate: LiAMMIS69 row: o column: 18
High quality sequence stop: 849.

Location/Qualifiers

Location/Qualifiers
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                         GAGGAGATTGTATTCGTTACTACCACAAACTCAGGATGTCTGCGGAGTACTCCCAGAGC
                                                                                                                ATCATGCTTCAAGGAGTGAGGGAGTCAGATGGAGGAAACTACACCTGCAGTATCCACCTA
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GAGGAGATTGTATTTCGTTACTACCACAAACTCAGGATGTCTGTGGAGTACTCCCAGAGC
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Pred. No. 7.4e-200;
0; Mismatches 6; Indels 4;
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/organism="Homo sapiens"
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Best Local Similarity 98.8%;
Matches 839; Conservative 0
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Homo sapiens
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                                                                             GGTTCCATCATGCTTCAAGGAGTGAGGAGTCAGATGGAGGAAACTACACCTGCAGTATC 120
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1079)
                                                                                                                                                                                                                                                                                                                                                                                     973 AAGAAGACCTGTGGAAATAAGAGTTCAGTGAATTCTACAGTCTTGGTGAAGAACACGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CACATTTACTCCCCAATAATTGTACGGGAGGTGATCGAGGAAGAAGAAGAACCAAGTGAAAAA
                                  GGTTCCATCATGCTTCAAGGAGTGAGGAGTCAGATGGAGGAAACTACACCTGCAGTATC
                                                                                                                                                181 CGAACACTGGTGACCCCGGCAGCCCTGAGGCCTCTGGTCTTGGGTGTAATCAGTTGGTG
                                                                                                                                                                                                                                                                                                                          241 ATCATTGTGGGAATTGTCTGTGCCACAATCCTGCTCCCTGTTCTGATATTGATCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                 301 AAGAAGACCTGTGGAAATAAGAGTTCAGTGAATTCTACAGTCTTGGTGAAGAACACGAAG
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                                                                                                                       CACCTAGGGAACCTGGTGTTCAAGAAACCATTGTGCTGCATGTCAGCCCGGAAGAGCCT
                                                                                                                                                                                                            CGAACACTGGTGACCCCGGCAGCCCTGAGGCCTCTGGTCTTGGGTGGTAATCAGTTGGTG
                                                                                                                                                                                                                                                                                                   ATCATTGTGGGAATTGTCTGTGCCACAATCCTGCTGCTCCCTGTTCTGATATTGATCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAGAGGCCACCTACATGACCATGCACCCAGTTTGGCCTTCTCTGAGGTCAGATCGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1213 AACTCACTTGAAAAAAGTCAGGTGGGGGAATGCCAAAAACACAGCAAGCCTTTTGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCAATACCACTGAAGATGGAGAATTTGGAGCCTGGCAAGAGAGACTGGGACAGCTCTGGA
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1537

318

1597

258

us-09-989-728-421.rst

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/clone='IMAGE:520788"
/lab_host='IMAGE:520788"
/lab_host='IMH08C|122"
/clone lib="WHH MGC|122"
/clone lib="WHH MGC|122"
/note="Organ: pooled lung and spleen; Vector: pcMV-SPORT6;
Site_1: Not1; Site_2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dr
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BI767696 790 bp mRNA linear EST 25-SEP-2001
603060652F1 NIH_MGC_122 Homo sapiens CDNA clone IMAGE:5209788 5',
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                                                                                                          437 GGAGCCTGGCAGAGAGACTGGACTGGAGCTCTGGAAGAACAGGCCTGCTGAGGGGAGGGGGGG
                                                                                                                                                                                                                                                                                                                                                        317 caaaccccccrircaarcagacccrccrcrcrcaggcraggricrragragaggriaacrcc
CGCTCTCCCAGCTGTCCTCTTTTTTTTTTTTACATACACTGAAGATGGAAATTT
                                                                                                                                                                            1478 ATGGACTTGGCCTCTGGAGTGGGACACTGGCCCTGGGAACCAGGCTGAGCTGAGTGGCCT
                                                                                                                                                                                                              1538 CAAACCCCCCCTTGGATCAGACCCTCTGTGGGCAGGGTTCTTAGTGGATGAGTTACTGG
                                                              GGAGCCTGGCAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGGAAGGGGAGG
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Pred. No. 8.3e-185;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                          1598 GAAGAATCAGAGATAAAAACCAACCCAAATCA 1629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   257 GAAGAATCAGAGATAAAAACCAACCCAAATCA 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 7
Location/Qualifiers
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98.98;
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Best Local S
Matches 782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGAGGTGATCGAGGAAGAAGCGAAGTGAAAATCAGAGGCCACCTACATGACCATGC 1177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CELL LINE) COT 25-NORMALIZED"
                                                                                                                       Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
Librariy was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6071.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?seq=cS0AL002BF04NP1&cluster=6071.r. Contact
http://www.genoscope.com/initrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0AL002BF04NP1.
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/cell line="RAMOS CELL LINE"
/clone lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
25-NORMALIZED"
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Pred. No. 5e-186;
7; Mismatches 21; Indels 3;
            Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length CDNA libraries and normalization Unpublished (2001)
Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.4%; Scor No. 5c. 96.2%; Pred. No. 5c. 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODL002YK08"
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CDNA Library preparation: Dr. M. Hunninghake, U of I cowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu Seq primer: M13 FORWARD
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llarity 99.7%; Pred. No. 1.8e-183;
Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="UI-H-FT1-bht-e-06-0-UI"
/tissue_type="Aveolar Macrophage"
                                                                                                                                                                                                                                                                                                                   1. .758
/organism="Homo sapiens"
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/db_xref="taxon:9606"
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                             AGTTGAGAGCAGCATGTTTGGCCCACTGAAACTCATCCTGCTGCCAGTGTTACTGGATT
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                                                              AAGTTGAGAGCAGCATGTTTTGCCCACTGAAACTCCATCCTGCTGCCAGTGTTACTGGATT
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UI-H-FT1-bht-e-06-0-UI 3', mRNA sequence.
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Email: cgapbs-r@mail.nih.gov
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

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Bonaldo, M.E., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene
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/dev stage="Adult"
/dev stage="Adult"
/lab_host="BH10B Life Technologies"
/clone_lib="NCI_CGAP_FT2"
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Itisue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.ulowa.edu/distribution/cgap.html
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                            279 GCTGTCCTCCTGTCTTCTTTGGTCAATACACTGAAGAAGAAGAAAATTTGGAGCCTGGC
                                                                                                                                                                                                                                                                      99 GTTGGATCAGACCCTCCTGTGGGCAGGGTTCTTAGTGGATGAGTTACTGGGAAGAATCAG
                                                                                   GCTGTCCTCCTGTCTTTGTTTTGGTCAATACACTGAAGATGGAGAATTTTGGAGCCTGGC
                                                                                                                                                                                                                                CCTCTGGAGTGGGACACTGGCCCTGGGAACCAGGCTGAGCTGAGTGGCCTCAAACCCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                      CCTCTGGAGTGGGACACTGGCCCTGGGAACCAGGCTGAGCTGAGCTGGCCTCAAACCCCCC
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/db_xref="taxon:9606"
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CD365542,1 GI:31149632
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CD365542/c
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KEYWORDS
SOURCE
ORGANISM
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DEFINITION

ACCESSION

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

FEATURES

ORIGIN

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/clone="INAGE:5173820"
/lab host="INAGE:5173820"
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pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age 69. Library is
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size arange 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
                                                                                                                   1416
                                                                                                                                                                                                                          1476
                                                                                                                                                                                                                                                                                                                            CATGGACTTGGCCTCTGGAGTGGGACACTGGCCCTGGGAACCAGGCTGAGCTGAGTGGCC 1536
     CAGCGGTGGAGACTCTCTCTGTGTGTGTCCTGGGCCACTCTACCAGTGATTTCAGACTC 1356
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603032387F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5173820 5',
                                                   350 cascesiseasacrerererererererereseseceaerereresearere 291
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tisgabs-rémail.nih.gov
Tisgabs-rémail.nih.gov
Tisgabs-rémail.nih.gov
Tisgabs-rémail.nih.gov
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Tisgabs-rémail.nih.gov
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Loud through the I.M.A.G.E. Consortium/LLNL at:
High quality sequence start: 8
High quality sequence stop: 739.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 800)
                                                                                                             CCGCTCTCCCCAGCTGTCCTCTTTTTTTTTTTTTTTACACTGAAGATGGAGAATT
                                                                                                                                                                                                                     TGGAGCCTGGCAGAGAGTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAG
                                                                                                                                                                                                                                                                                                                                                                    170 CATGGACTTGGCCTCTGGAGTGGGACACTGGCCTGGGAACCAGGCTGAGTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 TCAAACCCCCCGTTGGATCAGACCCTCCTGTGGGCAGGGTTCTTAGTGGATGAGTTACTG
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1597 GGAAGAATCAGAGATAAAAACCAACCCAAATCAA 1630
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JOURNAL
COMMENT
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BI818153
LOCUS
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KEYWORDS
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/wol_type="mRNA"
/wol_type="mRNA"
/db_xere="exacn:9606"
/clone="Ul-CF-EC1-ad2-a-24-0-UI"
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/dev stage="Adult and Feta!"
/dev stage="DH10B (Life Technologies) (Tl phage resistant)"
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modified polylinker; Site=1: EcoR I; Site=2: Not I;
/U-CF-EC1 is a normalized CDNA library containing the
following tissue(s): Normal lung from adult and from fetal
day 64, day 87, week 19 and week 42. The library was
constructed according to Banaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT773-Pac vector: The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
                                                                                                                Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cf.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGGGAATGCCAAAAACACAGCAAGCCTTTTGAGAAGAATGGAGAGTCCCTTCATCTCAG 1296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             966
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                                  2024 University of Iowa Med Labs, Iowa City, IA 52242, USA Tel: 319 356 4866
Fax: 319 356 7171
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Pred. No. 4.4e-173;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                 University of Iowa
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Best Local Similarity
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/urganism="Homo sapiens"
/mol type="mRNN"
/db zere="urganism="Nomo sapiens"
/db zere="urganism="Nomo sapiens"
/ds zere="urganism="nomo sapiens"
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327 GIGIGICCIGGGCCACTCTACCAGTGATTTCAGACTCCCGCTCTCCCAGCTGTCCTCCTG 268
       Contact: Robert Strausberg, Ph.D.
Email: cgapberramail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
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Pred. No. 9.1e-166;
0; Mismatches 5; Indels 0;
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al Similarity 99.3%;
666; Conservative C
Unpublished (1997)
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                                                                                                                                        TCCTTGGGCCTGAATGACTTGAATGTTTCCCCG-CTGAGCTAACAGTCCATGTGGGTGAT
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Pred. No. 1e-170;
0; Mismatches 8;
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Search completed: October 2, 2004, 05:02:57 Job time : 6335 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

October 1, 2004, 20:59:40; Search time 40 Seconds (without alignments) 947.487 Million cell updates/sec

US-09-989-728-422 2067 1 MFCPLKLILLEPVLLDYSLGL......RNNSLEKKSGGGMPKTQQAF 394 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	coxsackie- and ade	hypothetical prote	myelin PO protein	P0	-SVE	protei	channel		PO	PO	ch	vtoma-as	SHP substrate-1 pr		hypothetical prote	neural cell adhesi		Vrosi		50K glycoprotein p	thetical prot	hemicentin precurs	vascular endotheli	B-lymphocyte activ	secretory componen		rotein-tyrosin	μ	fasciclin II precu	•
SUMMAKTES		DI	JC7780	T08678	A32999	A61087	JC4776	138053	161783	JH0252	A29128	MPRTO	A57843	A53449	JC5288	A57638	T22889	T43027	836903	I58375	A54662	JC5519	T20992	T43290	JC4954	154766	QRHUGS	JL0118	A48999	A31923	A40114	
		Length DB					338 2						215				103						5175 2							33	86	
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RESULT 2 T08678

SHP substrate-1 nr	Down syndrome cell	T-cell receptor al	B-cell adhesion pr	BIG-1 protein - ra	perlecan precursor	elastic titin - hu	teratocarcinoma ql	connectin 3B - chi	vascular endotheli	junctional adhesio	pregnancy-specific	hypothetical prote	hebaran sulfate or	mveloid cell surfa	CON (CAL) CHECK CO
JC5289	T08851	A53268	JH0371	158164	A38096	I38346	A29915	PN0568	S51656	S56749	176668	T16525	S18252	A30521	206946
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ALIGNMENTS

RESULT 1 JC7780 COXBACKie- C/Species: C/Species: C/Acces: R/Thoelen, B/ACTERICE A/Reference A/ACOTENTE A/ACCESSION A/RESIGUES A/COMMENT: C/COMMENT:	RESULT 1 COXRACKIE- and adenovirus receptor - bovine C.Species: Bos primigenius taurus (cattle) C.Species: Bos primigenius taurus (cattle) C.Accession: JC7780 C.Accession: JC7780 C.Accession: JC7780 Biochem. Biophys. Res. Commun. 288, 805-808, 2001 A.Fitle: Characterization of a cDNA encoding the bovine coxsackie and adenovirus recepton contents: Liver A.Footents: Liver A.Footents
Query Ma Best Loc Matches	Query Match Best Local Similarity 23.9%; Pred. No. 1.1e-06; Matches 95; Conservative 61; Mismatches 146; Indels 96; Gaps 20;
oy Oy	5 LKLILLPVILDYSLGINDINVSPPELTVHVGDSALMGCVFQ-STEDKCIFKIDWTLSP 61 : : : :
oy G	62 GEHAKDEYVLYYYSNLSVPIGRFQNRVHL-MGDILCNDGSLLLQDVQEADQGTYICE 117 :: :
Qy	118 IRLKGESQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRA 177 :
oy GB	178 KE-EIVFRY-YHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCS 235
oy O	236 IHLGNLVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILI 295 :
& g	296 VKKTCGNKSSVNSTVLVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSE 355 1
& a	356 KSEATYMTWHPVWPSLRSDRNNSLEKKSGGGMPKTQ 391

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A;Title: Molecular cloning of cDNAs that encode the chicken Po protein: evidence for ear A;Reference number: A61087, MUID:90204597; PMID:1690817
A;Accession: A61087
A;Accession: A61087
A;Accession: A61087
A;Residues: Dot compared with conceptual translation
A;Residues: L249 cBAR>
C;Comment: This protein is found only in peripheral nervous system Schwann cells.
C;Superfamily: myelin P0 protein; immunoglobulin homology
C;Reywords: glycoprotein; myelin; Schwann cell; structural protein; transmembrane protein
F;129/Domain: signal sequence #status predicted cSIG>
F;30-149/Product: myelin P0 glycoprotein #status predicted cMAT>
F;30-153/Domain: extracellular #status predicted cEXT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 limbic-system-associated membrane protein precursor - human C;Species Homo sapiens (man) C;Species Homo sapiens (man) C;Species Homo sapiens (man) C;Species Homo sapiens (man) C;Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 19-May-2000 C;Accession: JC4776 #species 170, 189-195, 1996 #rection of the human limbic-system-associated A;Title: cDAA cloning and structural analysis of the human limbic-system-associated A;Titler: cDAA cloning and structural analysis of the human limbic-system-associated A;Titleference number: JC4776 MUID:96235133; PMID:8666243 A;Accession: JC4776 A;Molecule type: mRNA A;Residues: 1-338 <PIM> A;Accession: JC4776 A;Acce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Comment: This is a neuronal surface glycoprotein distributed in cortical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 RMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSI-HLGNLVFKKT-I 247
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                                                                                                  205 RVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGNLVFKKTIVLHVSPEEPRTLVTPAA 264
                                                                                                                                                                                                --K 147
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     --- GVPYIEKWGOFRG 95
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A;Gene: lamp
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor
C;Keywords: brain; glycoprotein; membrane protein; phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     myelin P0 glycoprotein precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 VVLHVLPEEPKELMVHVGGLIQMGCVFQSTE-VKHVTKVEWIFSGRRAKEEIVFRYYHKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ::|| :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19;
                                                                                                                                                                                                                                                                                                                                                            ---IVKKTCGNKSS 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 TLYVLEKVPTRY-----GVVLGS----IIGGVLLLVALLVAVVYLV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 VLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILI 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 249;
                                                                                                                                                           40 VGSDVTLYCGFWSNEYVSDLTTLSWRFRPDNSRDIISIFHYGN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;43-129/Domain: immunoglobulin homology <IMM>
F;154-179/Domain: transmembrane #status predicted <IMM>
F;180-249/Domain: intracellular #status predicted <IMT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.8%; Score 140.5; DB 1;
26.8%; Pred. No. 0.0014;
tive 34; Mismatches 70;
                                                                                                                                                                                                                                                                                                        265 LRPLVLGGNQLVIIVGIVCATILLLPVLIL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C,Accession: A61087
R,Barbu, M.
J. Neurosci. Res. 25, 143-151, 1990
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                                                                                                                                                                                                                                                                                                                                                                                                                148
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myelin PO protein precursor - horn shark
C;Species: Heterodontus francisci (horn shark)
C;Species: Heterodontus francisci (horn shark)
C;Species: Heterodontus francisci (horn shark)
C;Date: 10.Sep.1999 #sequence_revision 10.Sep.1999 #text_change 21-Jul-2000
C;Accession: A2299
R;Saavedra, R.A.; Fors, L.; Aebersold, R.H.; Arden, B.; Horvath, S.; Sanders, J.; Hood, J. Mol. Brol. 29, 149-156, 1989
A;Tetle: The myelin proteins of the shark brain are similar to the myelin proteins of th A;Reference number: A32999; MUID:90040744; PMID:2478717
A;Recession: A3299
A;Retures preliminary
A;Molecule type: mRNA
A;Residues: 1-246 <SAA
A;Cross-references: GB:X16714; NID:963976; PIDN:CAB37865.1; PID:94467434
C;Superfamily: myelin P0 protein; immunoglobulin homology
C;Keywords: glycoprotein; membrane protein; myelin; Schwann cell; structural protein
F;41-127/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               다
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271 QLVCMARNEGGEARLILQLTVLEPMEKPIFHDPISEK--ITAMAGHTISLNCSAAGTPTP 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGSLLLQDVQEADQGTYIC--EIRL-KGESQVFKKAVVLHVLPEEPKELMVHV--GGLIQ 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGCVFQSTEVKHVTKVEWIFSGRRAKBEIVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDI 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 FRNDGSIMLQGVRESDGGNYTCSIHLGNLVFKKTIVLHVSPEEPRTLVTP---AALRPLV 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              270 LGGNOLVI ---IVGIVCATIL-LLPVLILIVKKTCGNKSSV--NSTVLVKNTKKTNPEIK 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGSRKLIDCKAEGIPTPRVLWAFPEGVVLPAPYYGNRITVHGNGSLDIRSLRKS--DSV 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              324 EKPCHFERCEGEKHIYSPIIVREVIEE---EEP-SEKSBATYMTMHPV------WP 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                         Cispecies: Homo sapiens (man)
Cibate: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 23-Jul-1999
Cipate: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 23-Jul-1999
Cipatession: T08678
Riwambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, May 1999
A;Reference number: 216469
A;Accession: T08678
A;Accession: T08678
A;Molecule type: mRNA
A;Residues: 1-584 <WAM>A;Residues: 1-584 <WAM>A;Residues: 1-684 <WAM>A;Residues: 1-684 <WAM>A;Residues: 1-684 <WAM>A;Residues: 1-684 <WAM>A;Residues: 1-684 <WAM>A;Roberties: Cicate fetal brain; clone DKFZp564I1922
Cicateties: A;Note: DKFZp564I1922.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EHKEENDHKVFYGGDLKVDCVATGLPNPEISWSLPDGSLVNSFMQSDDSGGRTKRYVVFN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----SVPIGRFQNRVHLMGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 147; DB 2; Length 58; Pred. No. 0.0012; 68; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
               hypothetical protein DKFZp564I1922.1 - human (fragment)
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larity 26.0%; Pred. No. 0.00048;
Conservative 37; Mismatches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.18;
21.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLRSDRNNSLEKKSG 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 21.64
Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EHAKD-EYVLYYYSNL
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Best Local S:
Matches 44
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Sodium channel beta 2 subunit - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Ang-1996 #sequence_revision 12-Aug-1996 #text_change 05-Nov-1999
C;Accession: I61783
R;Isom, L.L.; Ragsdale, D.S.; DeJongh, K.S.; Westenbroek, R.E.; Reber, B.F.X.; Scheuer, 7
C[1] 83, 433-442, 1995
A;Title: Structure and Function of the Beta 2 Subunit of Brain Sodium Channels, a Transme A;Reference number: A57843; MuID:96067641; PMID:8521473
A;Reference number: A57843; MuiD:96067641; PMID:8521473
A;Reference number: A57843; MuiD:96067641; PMID:8521473
A;Accession: I61783
A;Accession: I61784
A;Accession: I617
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Nyelien Poptein protein zero
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence revision 06-Dec-1996 #text_change 16-Jun-2000
C;Accession: JH0252; JN0704; Ī39378; IS8118
R;Hayasaka, K; Nanao, K; Tahara, M:; Sato, W.; Takada, G.; Miura, M.; Uyemura, K.
Biochem. Biophys: Res. Commun. 180, 515-518, 1991
A;Title: Isolation and sequence determination of cDNA encoding the major structural prote
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A;Cross-references: GB:D10537; GB:D90501; NID:g220073; PIDN:BAA01395.1; PID:g22007
B;Cxporimental source: fetus spinal cord
R;Hayasaka, K.; Ohnishi, A.; Takada, G.; Fukushima, Y.; Murai, Y.
Biochem. Blophys. Res. Commun. 194, 1317-1322, 1993
A;Title: Mutation of the myelin Po gene in charcot-marie-tooth neuropathy type 1.
A;Reference number: JN0704; MUID:93356807; PMID:7688964
                                                                                                                                                                                                                                                                                     84 K---GQPYIDEVGTFKERIQWVGDPRWKDGSIVIHNLDYSDNGTFTCDVKNPPDIVGKTS 140
                                                                                                                                                                                                                                 247 -IVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVKKTCGNK-- 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 FONRVHLMGDILCNDGSLLLQDVQEADQGTYICEI----RLKGESQVFKKAVVLHVLPE 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QAIVVYT----DREVHGAVGSRVTLHCSFWSSEWVSDDISFTWRYQPEGGRDAISIFHYA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: EMBL: U37147; NID: g1086498; PIDN: AAB60506.1; PID: g1086499
                                                                                KLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGNLVFKKT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 PPELTVHVGDSALMGCVFQS--TEDKCIFKIDWTLSPGEHAKDEYVLYYYSN-LSVPIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----SSVNSTVLVKNTKKTNPEIKEKPCHFERC 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189 ALGRRLSAMEKGKLHKPGKDASKRGRQTPVLYAQC 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------LIQMGCVFQSTEVK
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les 44; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1-186 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Introns: 50/3; 120/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
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A; Molecule type: mRNA
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                                                                                88
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Matches
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                        F;333-338/Region: hydrophobic
F;40,66,136,148,279,287,300,315/Binding site: carbohydrate (Asn) (covalent) #status pred
F;42,115,142,164,171,220,231/Binding site: phosphate (Thr) (covalent) #status predicted
F;95,192,204,236,310/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Deje
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A;Status: preliminary; translated from GB/EWBL/DDBJ
A;Status: 1-251 cRES
A;Residues: 1-251 cRES
A;Cross-references: EMBL:Z31718; NID:g469516; PIDN:CAAB3513.1; PID:g469517
R;Su, Y:; Brooks, D.G.; Li, L.; Lepercq, J.; Trofatter, J.A.; Ravetch, J.V.; Lebo, Proc. Natl. Acad. Sci. US.A. 90, 10855-10860, 1993
Proc. Natl. Acad. Sci. US.A. 90, 10855-10860, 1993
A;Fille: Myelin protein zero gene mutated in Charcot Marie-tooth type 1B patients.
A;Reference number: A49643; MUID:94068501; PMID:7504284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 21-Jan-2000
C;Accession: 138053, A45643; S43191
C;Rccession: 138053; A45643; Sqrbhl, H.; Pfeiffer, R.A.; Van Broeckhoven, C. Hum. Mol. Genet. 3, 1701-1702, 1994
A;Title: Identification of a de novo insertional mutation in P0 in a patient with A;Reference number: 138053; MUID:95135435; PMID:7530550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --SLRIQKVDVYDE 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTYICEIRLKGESQVFXKAVVLHVLPE---EPKELMVHVGGLIQMGCVFQSTEV----K 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --RAKEEIVFRYYHKLRMSVEY----SQS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 HLTPTGREFEGEEEYLEILGITREQSGKYECKAANEVSSADVKOVKVTVNYPPTITESKS 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----WGHFQNRVNLVG--DIFRNDG--SIMLQGVRESDGG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227 NEATTGROASLKCEASAVPAPDFEWYRDDTRINSANGLEIKSTEGGSSLTVTNVTEEHYG 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 KAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTE-VKHVTKVEWIFSGRRAKEEIVFRYYH 187
                                                                                                                                                                                                                                                                                                                                                                                  4 PLKLILLPVLLDYSLGLN--DLNVSPPELTVHVGDSALMGCVFQSTEDK-----CIF 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 PLVLLRLCLLPTGLPVRSVDFNRGTDNITVRQGDTAILRCVLEDKNSKVAWLNRSGIIF 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231 NYTCSIHLGNLVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLL 289
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                                                                                                                                                                                                                         6.6%; Score 137; DB 2; Length 338;
20.1%; Pred. No. 0.0039;
tive 54; Mismatches 123; Indels 110;
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A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 50-105 < 5011>
A;Experimental source: peripheral blood
A;Note: sequence extracted from NCBI backbone (NCBIP:139777)
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A/Cross-references: GDB:125266; OMIM:159440
A/Map position: 1422-1423
C;Superfamily: myelin P0 protein; immunoglobulin homology
F;43-129/Domain: immunoglobulin homology <IMM>
sequence #status predicted <SIG>
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ilarity 23.7%; Pred. No. 0.0056;
Conservative 39; Mismatches 95
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                                                                                                                                                                                                                 Query Match
Best Local Similarity 20.1%
Matches 72; Conservative
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Best Local &
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C;Genetics:
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        Av30128
myelin PO protein - bovine
C;Species: Bos primigenius taurus (cattle)
C;Accession: A29128
R;Sakamoto, Y; Kitamura, K.; Yoshimura, K.; Nishijima, T.; Uyemura, K.
R;Sakamoto, Y.; Kitamura, K.; Yoshimura, K.; Nishijima, T.; Uyemura, K.
A;Title: Complete amino acid sequence of PO protein in bovine peripheral nerve myelin.
A;Title: Complete amino acid sequence of PO protein in bovine peripheral nerve myelin.
A;Title: Complete amino acid sequence of PO protein in bovine peripheral nerve myelin.
A;Mccession: A29128
A;Molecule type: protein
A;Mccession: A29128
A;Mccession: A29128
A;Molecule type: protein

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 KAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTE-VKHVTKVEWIFSGRRAKEEIVFRYYH 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 QAIVVYT----DREVHGAVGSRVTLHCSFWSSEWVSDDISFTWRYQPEGGRDAISIFHYA 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 QVTLYVFEKVPTRY-----GVVLGA-----VIGGVLGVVLLLLLFYVVR 180
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Best Local Similarity 26.2%; Pred. No. 0.0068;
Matches 42; Conservative 27; Mismatches 73; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cch 6.4%; Score 132; DB 1; al Similarity 26.2%; Pred. No. 0.0066; 45; Conservative 31; Mismatches 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S:
Matches 45,
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major structural protein of perip
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C;Superfamily: myelin PO protein; immunoglobulin homology
C;Superfamily: myelin PO protein; immunoglobulin homology
C;Superfamily: myelin; Schwann cell; structural protein; transmembrane protein; Steywords: glycoprotein; myelin; Schwann cell; structural protein; transmembrane protein; F;30-248/Product: myelin PO protein #status predicted <AID>
F;30-153/Domain: extracellular #status predicted <AID>
F;43-129/Domain: immunoglobulin homology <IMM>
F;154-179/Domain: transmembrane #status predicted <IMD>
F;180-248/Domain: intracellular #status predicted <IMD
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: O.Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: A57843
R;Isom, L.L.; Ragsdale, D.S.; DeJongh, K.S.; Westenbroek, R.E.; Reber, B.F.X.; Scheuer, A;Isom, L.L.; Ragsdale, D.S.; DeJongh, K.S.; Westenbroek, R.E.; Reber, B.F.X.; Scheuer, A;Itile: Structure and Function of the Beta 2 Subunit of Brain Sodium Channels, a Transm A;Reference number: A57843; MUID:96067641; PMID:8521473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              myelin PO protein precursor - rat

"Species: Rattus norvegicus (Norway rat)
C;Species: 10-62p-1897 #sequence_revision 30-Sep-1987 #text_change 18-Feb-1995
C;Accession: JQ6622; A22822
R;Lemke, G.; Lamar, B.; Patterson, J.
Neuron 1, 73-83, 1988
A;Title: Isolation and analysis of the gene encoding peripheral myelin protein zero. A;Reference number: JQ6622; MUID:90166482; PMID:2483091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Molecule type: mRNA
A,Residues: 1-248 <LEM2>
C,Comment: This protein is found only in peripheral nervous system Schwann cells.
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141 KELMVHVGGLIQMGCVFQSTE-VKHVTKVEWIFSGRRAKEEIVFRYYHKLRMSVEYSQSW 199
                                                                                                                                                                                                                                                                                                                               64 GTFKERIQWVGDPHRKDGSIVIHNLDYGDNGTFTCDVKNPPDIVGKTSQVTLYVFEKVPT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 AVVLHVLPEEPKELMVHVGGLIQMGCVFQSTE-VKHVTKVEWIFSGRRAKEEIVFRYYHK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189 LRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGNLVFKKT-- 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84
                                                                                                                     7 KEVHGAVGSQVTLYCSFWSSEWVSDDLSFTWRYQPEGGRDAISIFHYAK---GQPYIDEV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 AIVVYT----DREVYGAVGSQVTLHCSFWSSEWVSDDISFTWRYQPEGGRDAISIFHYAK
                                                                                                                                                                                                                                                200 GHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGNLVFKKT--IVLHVSPEEPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 IVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVK 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.3%; Score 130; DB 1; Length 248; Best Local Similarity 25.1%; Pred. No. 0.0094; Matches 43; Conservative 32; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        258 TLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 RY-----GVVLGA-----VIGGVLGVVLLALLLFYLIR 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-248 <LEM>
R;Lemke, G.; Axel, R.
Cell 40, 501-508, 1985
A;Title: Isolation and sequence of a cDNA encoding the nA;Reference number: A22822; MUID:85124601; PMID:2578885
A;Accession: A22822
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A,Molecule type: mRNA
A,Residues: 1-509 <YAM>
A,Cross-references: DDBJ:D87967, NID:g1864012, PIDN:BAA13520.1, PID:g1864013
C,Comment: This protein is a glycosylated receptor-like protein and plays a role in cell
acts as a docking protein and induce translocation of SHP-2 from the cytosol to the plas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1.1040 <DEV>
A;Cross-references: GB:U39761; NID:g1079711; PIDN:AAC46934.1; PID:g1079712
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homoloc
                        R'Yamao, T.; Matozaki, T.; Amano, K.; Matsuda, Y.; Takahashi, N.; Ochi, F.; Fujioka, Y.; Biochem. Biophys. Res. Commun. 231, 61-67, 1997
A;Title: Mouse and human SHPS-1: Molecular cloning of cDNAs and chromosomal localization A;Reference number: JC5287; MUID:97223399; PMID:9070220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor tyrosine kinase egl-15 precursor - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: OB-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 24-Sep-1999
C;Accession: A57638
R;DeVore, D.L.; Horvitz, H.R.; Stern, M.J.
A;DeVore, D.L.; Horvitz, Born, M.J.
A;Telle: An FGF receptor signaling pathway is required for the normal cell migrations of A;Reference number: A57638; MUID:96069862; PMID:7585964
                                                                                                                                                                                                                                                                                                                                                                                                                             24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 ----FKKAVVLHVLP----EEPKELMVHVGGLIQMGCVFQSTEV--KHVTKVEWIFSGRR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 AKEEIV-FRYYHKLRMSVEYSQSWGHFQNRVNLV--------GDIFRNDG 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 SPGEHAKDEYVLYYSNLSVPIGRFQNRVHLMGDILCN---DGSLLLQDVQEADQGTYIC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 VKFQKGPSEPDTEIQSGGGTEVYVLAKPSPPEVSGPADRGIPDQKVNFTCKSHGFSPRNI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300 PKNL--TKNTDGTYNYTSLFLVNSSAHREDVVFTCOVKHDO---OPALTRNHTVLGLAHS 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GN-----QLVIIVGIVCA--TILLLPVLILIVKKTCGNKSSVNSTVLVK 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     314 NTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEATYMTMHPVWPSLRS 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMLQGVRESDGG-NYTCSIHLGNLVFKKTIVLHVSPEEPRTLVTPAALR-PLVLG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 PLKLILLPVLLDYSLGL--NDLNVSPPELTVHV--GDSALMGCVFQSTEDKCIFKIDWTL
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                                                                                                                                                                                                                                                                                                                                                                                                                             165;
                                                                                                                                                                                                                                                                                                                                                                              Length 509;
                                                                                                                                                                                                                                                                                                                                                                                                                             64; Mismatches 162; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------EIRLKGESQV-------
                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                              6.1%; Score 125.5; DE 21.2%; Pred. No. 0.05;
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A; Status: preliminary
A; Molecule type: mRNA
                                                                                                                                            A, Accession: JC5288
                                                                                                                         A; Contents: Brain
                                                                                                                                                                                                                                                                                                                                   A; Map position: 2
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Matches 105;
                                                                                                                                                                                                                                                                                                          A; Gene: shps-1
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R;Connelly, M.A.; Grady, R.C.; Mushinski, J.F.; Marcu, K.B.
Proc. Natl. Acad. Sci. US.A. 91, 1337-1341, 1994
A;Title: PANG, a gene encoding a neuronal glycoprotein, is ectopically activated by intr
A;Reference number: A53449; MUID:94151325; PMID:8108413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-1028 <CON>
A;Residues: 18-1028 <CON>
A;Cross-references: GB:L01991; NID:g200056; PIDN:AAA17403.1; PID:g200057
C;Superfamily: contactin; fibronectin type III repeat homology; immunoglobulin homology
C;Keywords: glycoprotein
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                                                                                                                                                                                                                                                                                                                                                                          84 FONRVHLMGDILCNDGSLLLQDVQEADQGTYICEI-----RLKGESOVFKKAVVLHVLPE 138
                                                                                                                                                                                                                                                                                                                                                                                                       GTYTC----TAENQFGKANGTTHLVVTEPTRILAPSNMDVAVGESVILPC----QVQH 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----DSGMFQCIAENKHGLIYSSAELKVVASAPDFSRNPMKKNVQ 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -- LYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQ 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTYICEIRLKGESQVFKKAVVLHVLPEEPKELM------VHVGGLIQMGCVFQSTEVKH 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 VTKVE----WIFSGRRAKEEIVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIM 220
                                                                                                                                                                                                                                                                                     83
                                                                                                                                                                                                                                                                                                                              PITLSVLNGSDTRLPCTFNSCYTVNHKQFSLNWTYQECSNCSEEMFLQFRMKIINLKLER 94
A;Accession: A57843
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-215 <RES>
A;Cross-references: EMBL:U37026; NID:g1086496; PIDN:AAC52967.1; PID:g1086497
C;Genetics:
A;Gene: SCNB2
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C;Species: Mus musculus (house mouse)
C;Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-Sep-1999
                                                                                                                                                                                                                                                                                27 PPELTVHVGDSALMGCVFQS - TEDKCIFKIDWTLSPGEHAKDEYVLYYYSN-LSVPIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 SLGINDINVSPPELTVHVGDSALMGC-----VFQSTEDKCIFKI-DWTLSPGEHAKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---ALTDFKKDGSHFEK----VGG--SSSGDLM
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                                                                                                                                                                                                                                      21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.1%; Score 126; DB 2; Length 1028; 20.3%; Pred. No. 0.11; tive 49; Mismatches 91; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.Species: Mus musculus (house mouse)
C.Date: 25-Aug-1995 #sequence_revision 25-Aug-1995 #text_change
                                                                                                                                                                                      Length
                                                                                                                                                                                                                                    65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LQGVRESDGGNYTCSIHLG--NLVFKKTIVLHVSPEEPRTL 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plasmacytoma-associated neuronal glycoprotein PANG - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139 EPKELMVHVGG------LIQMGCVFQSTEVK 163
                                                                                                                                                                                   6.2%; Score 127.5; DB 2;
27.4%; Pred. No. 0.012;
Live 28; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     526 DPLLDIMFAWYFNG-----
                                                                                                                                                                                                                                 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Matches 43; Conserv
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Matches 57; Conserv
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A,Status: prelimina
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Introns: 30/1; 50/3; 104/3; 128/1; 245/1; 323/3; 403/3; 457/3; 493/3; 639/2; 665/3; 76
Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T22889
hypothetical protein F58A3.2 - Caenorhabditis elegans
C;Species: T3-012-1999 #sequence_revision 15-0ct-1999 #text_change 18-Feb-2000
C;Accession: T22889
R;Lennard, N.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19632
A;Reference number: Z19632
A;Reference number: DNA
A;Residues: 1-1103 <WIL>
A;Residues: 1-1103 <WIL>
A;Residues: 1-1103 <WIL>
A;Residues: clone F58A3.2
A;Reperimental source: clone F58A3
A;References: Cspeciferences: Clone F58A3
A;References: Cspeciferences: Clone F58A3
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                                                                                                                                                                                                                                                                                    309 TLKINCRAKGYPEPQIIWYKNGKMLKKSSARSGGYEFKF-----NRWSLEVEDAVVA 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VKHVTKVEWIFSGRRAKEEIVFRYYHKLRMSVEYSQSWGHFQN----RVNLVGDIFRNDG 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPHII---WV----RINKINGSYSYYN--NSAEEYMFNYTEMDTFDKAHVHHVGD----ES 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMLQGVRESDGGNYTC-----SIHLGNLVFKKTIVLH-VSPEEPRT-----LV 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  309 TLKLNCRAKGYPEPQIIWYKNGKMLKKSSARSGGYEFKF------NRWSLEVEDAVVA 360
                                                                                                                                                                                                                                               15 DYSL-----GLNDLNVS---PPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLSPGE
                                                                                                                                                                                                                                                                                                                                                                64 HAK-----DEYVLYYYSN----LSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEA
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                                                                                                                       6.1%; Score 125.5; DB 2; Length 1040; ilarity 19.9%; Pred. No. 0.12; Conservative 73; Mismatches 150; Indels 119;
                               protein kinase homology <KIN>
protein kinase ATP-binding motif
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                                                                                                                       Query Match
Best Local Similarity
Matches 85; Conserv
C; Keywords: ATP
F; 638-935/Domain:
F; 646-654/Region:
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366
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                                                                                                                                                                                                                                                                           261 TPAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVKKTCGNKSSVNSTV-LVKNTKKTN 319
                                                                                                                                                                                                                                                                                                            --VLPEEPKELMVHVGGLIQMGCVFQSTE 161
                                                                                           VKHVTKVEWIFSGRRAKEEIVFRYYHKLRMSVEYSQSWGHFQN----RVNLVGDIFRNDG
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Job time : 45 secs
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us-09-989-728-422.rsp

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GenCore version 5.1.6
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- protein search, using sw model OM protein ; Search time 25 Seconds (without alignments) 820.626 Million cell updates/sec 1, 2004, 20:51:10 ; October Run on:

US-09-989-728-422 2067 Perfect score:

1 MFCPLKLILLPVLLDYSLGL......RNNSLEKKSGGGMPKTQQAF 394 BLOSUM62 Scoring table: Sequence:

Gapop 10.0 , Gapext 0.5

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB s Maximum DB s Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	criptio	P78310 homo sapien	- 54			Homo sa		Q13449 homo sapien		Q9ers6 mus musculu	P25189 homo sapien	bos	P27573 mus musculu			h x-		Q8spv8 pan troglod	Q10656 caenorhabdi		Q96pq1 homo sapien	mus mu		pan t	homo	pan t	3 homo	3 homo	'n	-		O60487 homo sapien	7797	P59823 mus musculu
SUMMARIES	ID	CXAR HUMAN	MYPO HETFR	CXAR MOUSE			EVA1 MOUSE	LAMP HUMAN	LAMP_RAT	IPL2_MOUSE	MYPO_HUMAN	MYP0_BOVIN	MYPO_MOUSE	MYPO_RAT	A33_HUMAN	IPL2_HUMAN	CIB2_RAT	FCGA_PANTR	EG15_CAEEL	FCG2_RAT	SILL_HUMAN	VGR3_MOUSE	LAMP_CHICK	SILL PANTR	IPL1_HUMAN	IPL1_PANTR	PIGR_HUMAN	FCGA HUMAN	VGR3_HUMAN		FAS2_SCHAM		SHS1_MOUSE	IPL1_MOUSE
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											Q9ny72 homo sapien
DSCA_HUMAN	JAM1 BOVIN	SIL8 HUMAN	IPL1_RAT	PGBM HUMAN	CEPU_CHICK	NEO1 MOUSE	EMB MOUSE	CIB3 MACFA	FPRP HUMAN	NFAS HUMAN	CIB3_HUMAN
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2012	298	499	969	4391	353	1493	330	215	879	1240	215
5.6	5.6	9.5	5.6	5.5	5.4	5.4	5.3	5.3	5.3	5.3	5.3
116	115.5	115.5	115	113.5	112	112	110.5	110	109.5	109.5	109
34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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SEQUENCE FROM N.A.

MEDLINE=97250541; PubMed=9096397;
Tromko R.P., Xu R., Philipson L.;
"HCAR and MCAR: the human and wuse cellular receptors for subgroup C adenoviruses and group B coxsackieviruses.";
Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).
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MEDLINE=22388257; PubMed=12477932;
Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Straubberg R.L., Reingold B.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
                                                                                                                               Б
                                                                                                                                                                                                                                                                         MEDLINE=97190109; PubMed=9036860; MEDLINE=97190109; PubMed=9036860; Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.; "Isolation of a common receptor for Coxsackie B viruses and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mizra M.,
                             CXAR HUMAN STANDARD; PRT; 365 AA.
PY310; 006694;
30-MAY-2000 (Rel. 39, Last sequence update)
10-MCT-2003 (Rel. 42, Last annotation update)
Coxsackievirus and adenovirus receptor precursor (Coxsackievirus adenovirus receptor) (CVB3 binding protein).
CXADR OR CAR.
                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Andersson B., Tomko R., Andersson K., Darban H., Oncu D., Mizza M
Sollerbrant K., Sonnhammer B., Philipson L.;
"Putative regulatory domains in the human and mouse CAR genes.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genomic organization and chromosomal localization of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anderson C.W., Kieleczawa J., Dunn J.J., Freimuth P.; "Sequence and expression of CXADR, the human gene for the coxsackievirus and adenovirus receptor."; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bowles K.R., Gibson J., Wu J., Shaffer L.G., Towbin J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coxsackievirus B-adenovirus receptor gene.";
Hum. Genet. 105:354-359(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=20008750; Pubmed=10543405;
                                                                                                                                                                                                                                                                                                                                                                       adenoviruses 2 and 5.";
Science 275:1320-1323(1997).
                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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RESULT 1
CXAR HUMAN
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Carainci P., Prange C.,

Brownstein M.J., Usdin T.B., Toshiyuik S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rabask S.A., McKwarnan R.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W.,

Nhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield V. Schein J.E., Jones S.J.M., Marra M.A.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

Human and mouse cDNA sequences.", Jone than 15,000 full-length

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

- FUNCTION: SERVES AS A RECEPTOR FOR GROUP B COXSACKIEVIRUSES AND

SUBGRROUP C OF ADENOVIRUSES (ADZ AND ADS).

- SUBICRELUTAR LOCATION: Type I membrane protein.

- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50835; IG_LIKE; 2.
Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
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IG-LIKE C2-TYPE 2.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AP169361, AAF05908 11, JOINED.
AP169362, AAF05908 11, JOINED.
AP169363, AAF05908 11, JOINED.
AP169364, AAF05908 11, JOINED.
AP169365, AAF05908 11, JOINED.
AF200465, AAF24344 11, --
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Genew; HGNC:2559; CXADR.
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PDB; 1F5W; 08-NOV-00.
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SIGNAL 1
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SMART; SM00408; IG
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8.1%; Score 168; DB 1; Length 365;

Query Match

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                                                                                                                              62 GEHAKDEYVLYYSNLSVPIGRF---QNRVHL-MGDILCNDGSLLLQDVQEADQGTYICE 117
                                                                                                                                                    118 IRLKGESQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVF----QSTEVKHVTKVEWIFS 173
                                                                                                                                                                                                                                174 GRRAKEEIVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYT 233
                                                                                                                                                                                                                                                                                                                   211
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                                                                                                                                                                                                                                                                                                                                                                                          CTVR--NRVGSDQCLLRLNVVPP-----SNKAGLIAGAIIGTLLALALIG 254
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                                                                             5 LKLILLPVLLDYSLGLNDLNVSPPELTVH--VGDSALMGCVFQ-STEDKCIFKIDWTLSP
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                 Gaps
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10-OCT-2003 (Rel. 42, Last annotation update)
Myelin PO protein precursor (Myelin protein zero) (Myelin peripheral protein) (MPP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-50040744; PubMed=2478717;
Saavedra R.A., Fors L., Aebersold R.H., Arden B., Horvath S.,
Sanders J., Hood L.;
The myelin proteins of the shark brain are similar to the myelin
proteins of the mammalian peripheral nervous system.";
J. Mol. Bvol. 29:149-156(1989).
I. FUNCTION: Creation of an extracellular membrane face which guide
the wrapping process and ultimately compacts adjacent lamellae.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Found only in peripheral nervous system
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21.8%; Pred. No. 2e-06;
tive 65; Mismatches 148; Indels 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schwann cells.
-!- PTM: N-GLYCAN IS SULFATED (BY SIMILARITY).
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Belongs to the myelin PO protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPKSRTSTARSY----IGSNHSSLGSMSPSNMEGYSKTQ 317
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                   Conservative
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 Best Local Similarity
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                                                                                                                                                                                                                                                                               95
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                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97190109; PubMed=8036860;
Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones B.,
Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;
"Isolation of a common receptor for Coxsackie B viruses and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryotana (2008)
Eukaryotan Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                     CXAR MOUSE STANDARD; PRT; 365 AA.
P97792; 009052;
30-MAY-2000 (Rel. 39, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Coxsackievirus and adenovirus receptor homolog precursor (mCAR)
HSSP, P06907; INEU.
R HSSP, P06907; INEU.
R InterPro; IPR007110; Ig-like.
R InterPro; IPR00320; Myelin.
DR InterPro; IPR00320; Myelin.
DR RINITS; PR00213; MYELINPO.
DR RART; SM04406; IGV: 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS00568; MYELIN PO; 1.
DR Wyelin; Structural protein; Glycoprotein; Transmembrane; Myelin; Structural protein; Glycoprotein; Signal.
TYNAL 27 MYELIN PO PROTEIN.
TYNAL 27 MYELIN PO PROTEIN.
                                                                                                                                                                                                                                                                                                                                      265 LRPLVLGGNQLVIIVGIVCATILLLPVLIL------IVKKTCGNKSS 305
                                                                                                                                                                                                                                                                                                                                                . .) (COMPLEX)
                                                                                                                                                                                                                    7.1%; Score 146.5; DB 1; Length 246; 26.0%; Pred. No. 7e-05;
                                                                                                                                                                                                                                        61; Indels
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                                                                                                                                                   CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            adenoviruses and group B coxsackieviruses.";
Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).
                                                                                                                                                                     POTENTIAL,
N-LINKED (GLCNAC.
                                                                                                                                                             IG-LIKE V-TYPE
                                                                                                                                                                                                                                       37; Mismatches
                                                                                                                                                                                          SIMILARITY)
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STRAIN-C57BL/6J; TISSUE=Liver;
MEDLINE=98080429; PubMed=9420240;
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                                                                                                                                                                                                   246 AA; 27335 MW;
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                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 SDNQIVDQVIILYSGDKIYDNYYPDLKGRVHFTSNDVKSGDASINVTNLQLSDIGTYQCK 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 V--KKAPGVANKKFLLTVL-VKPSGTRCFVDGSBEIGNDFKLKCEPKEGSLPLQFEW--- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 GRRAKEEIVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYT 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---IREDVP 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VAAPNLSRMGAVPVMIPAQSKDGSIV -> FKYAYKTDGIT
VV (IN REF. 2 AND 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 LKLILLPVLLDYSLGLNDLNVSPPELTVH - - VGDSALMGCVFQ - STEDKCIFKIDWTLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mmunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.1%; Score 146; DB 1; Length 365;
11.8%; Pred. No. 0.00013;
ve 58; Mismatches 155; Indels 100; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
Bergelson J.M., Krithivas A., Celi L., Droguett G., Horwitz M.S., Wickham T., Crowell R.L., Finberg R.W.; "The murine CAR homolog is a receptor for coxsackie B viruses and
                                                                                                                       J. Virol. 72:415-419(1998).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5445B4B52A34B2A2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          254 GAILFCC------HRKRREEKYEKEVHHD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      354 SEKSEATYMTMHPVWPSLRSDRNN--SLEKKSGGGMPKTQ 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Embl. 11201699, Cxadr. InterPro; IPR007110; Ig-like. InterPro; IPR007110; Ig-like. Pfam; PF0047; Ig. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00408; IGC2; 1.
PROSITE; PS50835; IG_LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Y10320; CAA71368.1; -. EMBL; U90715; AAC53148.1; -. EMBL; Y11929; CAA72679.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.8%;
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365
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--GQPYIDDVGSFKERMEWVGNPRRKDGSIVIHNLDYTDNGTFTCDVKNPPDIVGKSSQV 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 RMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSI-HLGNLVFKKT-I 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               evidence for early expression in avians.";
J. Neurosci. Res. 25:143-151(1990).
-!- FUNCTION: Creation of an extracellular membrane face which guides the wrapping process and ultimately compacts adjacent lamellae.
-!- SUBCELLUTAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: Found only in peripheral nervous system
                                                                                                                                                                                                                                                                    01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-2003 (Rel. 42, Last annotation update)
Myelin PO protein Precursor (Myelin protein zero) (Myelin peripheral protein) (MPP)
Drotein) (MPP)
BLUIN gallus (Chicken)
Archosauria; Aves; Neognathae; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 LAIHVY - - TPREVYGTVGSHVTLSCSFWSSEWISBDISYTWHFQAEGSRDSISIFHYGK -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular cloning of cDNAs that encode the chicken PO protein:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248 VLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILI 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inter-
In
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283 PPKSRTSTARSY----IGSNHSSLGSMSPSNMEGYSKTQ 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.8%; Score 140.5; DB 1;
26.8%; Pred. No. 0.00022;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG-LIKE V-TYPE. POTENTIAL.
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MEDLINE=90204597; PubMed=1690817;
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                                                                                                                                                                                               STANDARD;
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Best Local Similarity
Matches 45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
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ID _CIB2_HUMAN
                                                                                                                                                                                               CHICK
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P37301:
                                                                                                                                                          CHICK
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Bolino A., Seri M., Caroli F., Eubanks J., Srinivasan J., Mandich P., Schenone A., Quattrone A., Romeo G., Catterall W.A., Devoto M.; "Exclusion of the SCN2B gene as candidate for CMT4B."; Eur. J. Hum. Genet. 6:622-634(1998).
                                                                                                                                                                                          Bubanks J., Srinivasan J., Dinulos M.B., Disteche C.M., Catterall W.A.; "Structure and chromosomal localization of the beta2 subunit of the
                                                                                                                                                                                                                                                                                                                                                                                      SECUENCE FROM N.A.
Isom L.L., Mattei L.N., Ragsdale D.S.;
IPrimary structure and functional expression of a beta 2 subunit of human infant brain sodium channels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human and mouse CDNA Sequences.;

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)

-!- FUNCTION: Crucial in the assembly, expression, and functional modulation of the heterotrimeric complex of the sodium channel. The beta-2 subunit causes an increase in the plasma membrane surface area and in its folding into microvilli (By similarity).
-!- SUBUNIT: THE SODIUM CHANNEL CONSISTS OF A PORE-FORMING ALPHA SUBUNIT: BETA-1 AND BETA-2 SUBUNITS. BETA-1 IS NONCOVALENTLY ASSOCIATED WITH ALPHA, WHILE BETA-2 IS COVALENTLY LINKED BY DISULFIDE BONDS (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cruz J.S., Santana L.F., Frederick C.A., Isom L.L., Malhotra Mattei L.N., Kass R.S., Xia J., An R.-H., Lederer W.J.; Whether 'slip-mode conductance' occurs."; Science 284:711-711(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
060939; 075302; Q9UNN3;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-0AR-2004 (Rel. 43, Last annotation update)
                                                         Sodium channel beta-2 subunit precursor.
                                                                                                                                                                                MEDLINE=97439560; PubMed=9295116;
                                                                                                                                                                                                                                                                                                       MEDLINE=99104330; PubMed=9887383;
                                                                                                                                                                                                                                     human brain sodium channel.";
NeuroReport 8:2775-2779(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                     FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Heart;
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                                                                                                                                                                    TISSUE-Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 TLSPGEHAKDEYVLYYYSNLSVPI-GRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYIC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 BIR----LKGESQVFKKAVVLHVLP-EEPKELMVHVGGLIQMGCVFQSTEV--KHVTKVE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVLPLLL--SLQLTAL--CPTEAVEIYTSGALEAVNGTDVRLKCTFSSFAPVGDALTVTW 63
                                                                                                                                                                                               MEDILNE=9852857; PubMed=958423;
Guttinger M., Sutti F., Panigada M., Porcellini S., Merati B.,
Guttinger M., Sutti F., Panigada M., Porcellini S., Merati B.,
Mariani M., Teealu T., Consalez G.G., Grassi F.,
Epitbelial V-like antigen (EVA), a novel member of the immunoglobulin
superfamily, expressed in embryonic epithelia with a potential role as
homotypic adhesion molecule in thymus histogenesis.",
Cell Biol. 141:1061-1071(1998).
-!- FUNCTION: Mediates homophilic cell-cell adhesion.
-!- FUNCTION: Mediates homophilic cell-cell adhesion.
-!- SUBCELDUAR LOCATION: Type I membrane protein (Probable).
-!- TSUS ESCIFICITY: Expressed in liver and gut, skin, and testis
but not in thymocytes, lymphocytes, macrophage or dendritic cells
or cell lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMARY; SN00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Cell adhesion; Immunoglobulin domain; Transmembrane; Glycoprotein;
                                                                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBL TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IG-LIKE V-TYPE.

BY SIMILARITY.

N-LINKED (GLCNAC. .) (POTENTIAL)

N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 27.1%; Pred. No. 0.00036; Similarity 27.1%; Pred. No. 0.00036; 77; Conservative 33; Mismatches 92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 ILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPITHELIAL V-LIKE ANTIGEN 1.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F6E5E36787CE69D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL. CYTOPLASMIC (POTENTIAL).
        10-OCT-2003 (Rel. 42, Last annotation update) Epithelial V-like antigen 1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WI-----FSGRRAKEEIVFRYYHKLRMSVE 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF030454; AAC40128.1; -. HSSP; P06907; INEU. MGD; MG1:1289160; Bva. InterPro; IPR007110; Ig-like. InterPro; IPR003596; Ig-v. InterPro; IPR00920; Myelin_P0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24162 MW;
                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=RAG-2; TISSUE=Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 1.
PRINTS; PR00213; MYELINPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57; Conservative
                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47 1
39
118 1
215 AA;
                                              EVA1 OR EVA.
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SIGNAL
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                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 FONRVALMGDILCNDGSLLLQDVQEADQGTYICEI----RLKGESQVFKKAVVLHVLPE 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 PPELITVHVGDSALMGCVFQS--TEDKCIFKIDWTLSPGEHAKDEYVLYYYSN-LSVPIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50835; IG_LIKE; 1.
IONIC channel; Transmembrane; Ion transport; Voltage-gated channel;
Glycoprotein; Signal; Immunoglobulin domain; Sodium channel.
SIGNAL
1 29 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
H -> Q (IN REF. 1).
T -> N (IN REF. 1).
T -> N (IN REF. 1).
T -> S (IN REF. 1).
S -> F (IN REF. 1).
-!- TISSUE SPECIFICITY: Brain specific.
-!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.7%; Score 138.5; DB 1; Length 215; 29.2%; Pred. No. 0.00027; ive 25; Mismatches 60; Indels 29,
                                                                                                                                                                                                                                                                                                                                                GENEW; HGNC: 10589; SCR2B.

MIN, 601327; -.

MIN, 601327; -.

MIN, 601327; -.

MIN, 601327; -.

GO; GO:0005248; P:svoltage_gated sodium channel activity; TAS.

GO; GO:0005268; P:synaptic transmission; TAS.

InterPro; IPR007110; Ig-like.

InterPro; IPR000359; Ig.

InterPro; IPR000359; Ig.

FRINTS; PR00013; MYELINPO.

SMART; SM00409; IG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
SODIUM CHANNEL BETA-2 SUBUNIT.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94A30A60A32683F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 EPKE-----LMVHVGG-----LIQMGCVFQSTEVK 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPPERDSTVAVIVGASVGGFLAVVILVLMVVKCVRRKKEQK 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IG-LIKE C2-TYPE POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 41, Created)
(Rel. 41, Last sequence update)
                                                                                                                                                                                                               EMBL, AF007783; AAC26013.1; -.
EMBL, AF04949; AAC05274.1; -.
EMBL, AF04949; AAC05208.1; JOINED.
                                                                                                                                                                                                                                                                                         24326 MW;
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28-FEB-2003
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070255;
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                         SEQUENCE
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                                                Query Match
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                                                                                                                                                                                                                                                                              Gene 170:189-195(1996)
-!- FUNCTION: MEDIATES SELECTIVE NEURONAL GROWTH AND AXON TARGETING.
CONTRIBUTES TO THE GUIDANCE OF DEVELOPING AXONS AND REMODELING OF
MATURE CIRCLITS IN THE LIMBIC SYSTEM. ESSENTIAL FOR NORMAL GROWTH
OF THE HYPPOCAMPAL MOSSY FIBER PROJECTION (BY SIMILARITY).
-!- SUBSCELLUITS LOCATION: Attached to the membrane by a GPI-anchor.
-!- TISSUE SPECIFICITY: Expressed on limbic neurons and fiber tracts
as well as in single layers of the superior colliculus, spinal
chord and cerebellum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FROUED IN MATURE FORM (POTENTIAL).
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
POTENTIAL.
POTENTIAL.
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI TaxID=9606;
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=96235133; PubMed=8666243;
Pimenta A.F., Fischer I., Levitt P.;
"cDNA cloning and structural analysis of the human limbic-system-associated membrane protein (LAMP).";
                                                                                                                                                                                                                                                                                                                                                                                        chord and cerebellum. SIMILARITY: Belongs to the immunoglobulin superfamily. IgLON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM; 603241; -.

GO; 00007399; P:neurogenesis; TAS.

InterPro; IPR00310; Ig-like.

InterPro; IPR003598; Ig_c2.

Pfam; PF00047; ig; 3.

SMART; SM00408; IGc2; 2.

PROSITE; PSS0835; IG_LIKE; 3.

Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor; Repeat; Signal; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
LIMBIC SYSTEM-ASSOCIATED MEMBRANE
                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Limbic system-associated membrane protein precursor (LSAMP).
                                                                338 AA
 183 WADRADKAEGTKSKEEEKLNQGNKVSVFVE 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U41901; AAC50569.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew; HGNC: 6705; LSAMP.
                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111
197
290
                                                                                                                                                       (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; JC4776; JC4776
                                                                                                                                          LSAMP OR LAMP.
                                                                                                                                                         Homo sapiens
                                                                 HUMAN
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                                                    HUMAN
                                                                 LAMP
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----SLRIQKVDVYDE 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 HLTPTGREFEGEEEYLEILGITREQSGKYECKAANEVSSADVKOVKVTVNYPPTITESKS 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --WGHFQNRVNLVG--DIFRNDG--SIMLQGVRESDGG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       227 NEATTGRQASLKCEASAVPAPDFEWYRDDTRINSANGLEIKSTEGGSSLTVTNVTEEHYG 286
                                                                                                                                                                                                                                                                                                                                                                        72
                                                                                                                                                                                                                                                                                                     4 PLKLILLPVLLDYSLGLN--DLNVSPPELTVHVGDSALMGCVFQSTEDK-----CIF 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              287 NYTC-----VAANKLGVINAS----LVLERPGSVRG-INGSISLAVPLMLLAASLLCL 334
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-i - FUNCTION: MEDIATES SELECTIVE NEURONAL GROWTH AND AXON TARGETING.

-i - FUNCTION: MEDIATES SELECTIVE NEURONAL GROWTH AND AXON TARGETING.

CONTRIBUTES TO THE GUIDANCE OF DEVELOPING AXONS AND REMODELING OF MATURE CIRCUITS IN THE LIMBIC SYSTEM. BSSENTIAL FOR NORMAL GROWTH OF THE HYPPOCAMPAL MOSSY FIBER PROJECTION.

-i - SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.

-i - SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.

-i - SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.

-i - SUBCELLULAR LOCATION: Attached to the membrane opposition in cognition, emotion, memory, and learning.

-i - DETECTED IN PRESUMPTINE CORTEX, MEDIAL LIMBIC AREAS OF THE THALAMUS AND HYPOTHALAMUS. IN THE ADULL, IT IS FOUND IN HYPOTHALAMUS. IN THE ADULL, IT IS FOUND IN HYPOTHALAMUS. IN THE ADULL, IT IS FOUND IN HYPOTHALAMUS.
                                                                                                                                                                                                                                                                                                                                                                        PLVLLRLLCLLPTGLPVRSVDFNRGTDNITVRQGDTALLRCVLEDKNSKVAWLNRSGIIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUB=Hippocampus;
MEDLINE=95374785; PubMed=7646886;
Pimenta A.F., Zhukareva V., Barbe M.F., Reinoso B.S., Grimley C.,
Henzel W., Fischer I., Levitt P.;
"The limbic system-associated membrane protein is an Ig superfamily
member that mediates selective neuronal growth and axon targeting.";
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Belongs to the immunoglobulin superfamily. IgLON
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                                                                                                                                                                                                                         54; Mismatches 123; Indels 110;
GPI-anchor amidated asparagine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Limbic system-associated membrane protein precursor (LSAMP)
                                                                                                                                              Length 338;
                                                                       03455F286DF5D92F CRC64;
                                                                                                                                              . Match 6.6%; Score 137; DB 1;
Local Similarity 20.1%; Pred. No. 0.00065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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                                       (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 AGHDKWSLDPRVBLEKRHSLEY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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01-NOV-1997 (Rel. 35, Last seq
10-OCT-2003 (Rel. 42, Last ann
                                                                           338 AA; 37308 MW;
                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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   315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |:| | :: : | : ::: | | : : :: | | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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(POTENTIAL).
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InterPro; IPR007110; Ig-like.
InterPro; IRR003598; Ig_c2.
Pfam; PF00047; ig; 3.
SWART; SW00408; IGc2; 2.
PROSITE; PS50835; IG_LIKE; 3.
Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor; SIGNAL 1. 28
                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN.
REMOVED IN MATURE FORM (POTENTIAL)
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.5%; Score 135; DB 1; Length 338;
19.8%; Pred. No. 0.00095;
ative 55; Mismatches 123; Indels 110;
                                                                                                                                                                                                                                                                                                                                                                                       LIMBIC SYSTEM-ASSOCIATED MEMBRANE
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10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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ID _IPL2_MC
AC _Q9ERS6;
DT __10-OCT-
DT __10-OCT-
DT __10-OCT-
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                                                                                                                                                                                                                                                                                                                                                                                                                                        "Identification and characterization of two members of a novel class of the interleukin-1 receptor (IL-IR) family. Delineation of a new class of IL-IR-related proteins based on signaling."; J. Biol. Chem. 275:29946-29954 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isold-Q9ERS6-2; Sequence=VSP 008056, VSP 008057;
Note=may be due to an intron_retention;
ISSUE SPECIFICITY: Detected in fetal brain after day 12.5, in particular in parts of the diencephalon and in the basal plate of the spinal cord. In postnatal brain detected in cerebral cortex, olfactory bulb, in the CA1 region of the hippocampus and in Purkinje calls of the Xth cerebellar lobule.

SIMILARITY: Belongs to the interleukin-1 receptor family.
SIMILARITY: Contains 1 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              central
X-linked interleukin-1 receptor accessory protein-like 2 precursor
                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO1539; INTRLEUKNIR2.
PRINTS; PRO1537; INTRLEUKNIR1F.
SMART; SMO0255; TIR; 1.
PROSITE; PS50804; TIR; 1.
PROSITE; PS50104; TIR; 1.
Receptor; Repeat; Signal; Transmembrane; Immunoglobulin domain;
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
TISSUB-Brain, and Liver;
MEDLINE=20459050; PubMed=10882729;
Born T.L., Smith D.E., Garka K.E., Renshaw B.R., Bertles J.S., Sims J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ferrante M.I., Ghiani M., Bulfone A., Franco B.;
"ILIRAPL2 maps to Xq22 and is specifically expressed in the
nervous system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 2), AND TISSUE SPECIFICITY
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EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q9ERS6-1; Sequence=Displayed;
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InterPro; IPR007110; Ig-like.
InterPro; IPR004075; II, receptor1.
InterPro; IPR004075; IL1 receptor1.
InterPro; IPR004077; IL1 receptor1Ip.
Pfam; PF00047; IG1.
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                            (ILIRAPL-2 related protein) (TIGIRR-1) ILIRAPL2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene 275:217-221(2001).
                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                NCBI TaxID=10090;
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355
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Biophys. Res. Commun. 180:515-518(1991)
                                                                   type 1.";
Biochem. 1
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                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P25189; Q16072; Q92677; Q9BR67; 01-MAY-1992 (Rel. 22, Created) 01-MAY-1992 (Rel. 22, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) 10-OCT-2003 (Rel. 42, Last annotation update) 10-OCT-2003 (Myelin protein precursor (Myelin protein zero) (Myelin peripheral protein) (MPP).
                                                                                N-LINKED (GLCNAC. ) (POTENTIAL)
N-LINKED (GLCNAC. ) (POTENTIAL)
N-LINKED (GLCNAC. ) (POTENTIAL)
N-LINKED (GLCNAC. ) (POTENTIAL)
DLIYK -> GILFS (in isoform 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Uyemura K.; "Isolation and sequence determination of cDNA encoding the major structural protein of human peripheral myelin.";
                                                                                                                                                                                                60; Mismatches 130; Indels 114;
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                                                                                                                                                                             Length 686;
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                            36160D1CDE9B8264 CRC64;
  (POTENTIAL)
                                                                                                                                /FTId=VSP 008056.
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          IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
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                                                                                                                                                            78797 MW;
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Best Local Similarity 20.4%;
Matches 78; Conservative 6
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DISULFID
DISULFID
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As Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Attausher R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Attachul S.P., Zeeberg B. Buetow K.H., Schaefer C.F., Bhar N.K.,

Attachul S.P., Zeeberg B. Buetow K.H., Schaefer C.F., Bhar N.K.,

An Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Rapleton M., Soares M.B., Mockens M.F., Casavant T.L., Scheetz T.E.,

Rapleton M.J., Usdin T.B., Toochiyuki S., Carninci P., Prange C.,

Rapleton M.J., Wokernan K.J., Marasnon R.D., Mullahy S.J.,

Rapleton B.K., McKernan K.J., Marasnon R.D., Hulyk S.W.,

Rapleton B.K., Muray D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rapleton B.K., Maray D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rapleton B.K., Coultman J.W., Green E.D., Dickson M.C.,

Rapleton M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Rapleton B.K., Chimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rapleton and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.
Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.
Phelan M., Farmer A.;
"Cloning of human full-length CDSs in BD Creator(TM) system donor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Linkage and mutation analysis in an extended family with Charcot
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REDILINES4302675; PubMed=7518101;
Patel P.1., Lupski J.R.,

"Charcot-Marie-Tooth disease: a new paradigm for the mechanism of
SEQUENCE FROM N.A., AND VARIANT CMTIB HIS-98.
TISSUE-Spinal cord;
TISSUE-93156807, PubMed-7688964;
Hayasaka K., Ohnishi A., Takada G., Fukushima Y., Murai Y.,
"Mutation of the myelin P0 gene in Charcot-Marie-Tooth neuropathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pham-Dinh D., Fourbil Y., Blanquet F., Mattei M.-G., Roeckel N.,
Latour P., Chazot G., Vandebberghe A., Dautigny A.;
"The major peripheral myelin protein zero gene: structure and
localization in the cluster of Fc gamma receptor genes on human
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MEDLINE=95282670; PubMed=7762451;
ROA Bls., Lupski, J.R.;
"Molecular genetics of Charcot-Marie-Tooth neuropathy.";
Adv. Hum. Genet. 22:117-152(1994).
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Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Nelis E., Timmerman V., De Jonghe P., Muylle L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosome 1q21.3-q23.";
Hum. Mol. Genet. 2:2051-2054(1993).
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MEDLINE=99103460; PubMed=9888385;
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Van Broeckhoven C.;
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Hayasaka K., Himoro M., Sato W., Takada G., Uyemura K., Shimizu N.,
Bird T.D., Conneally P.M., Chance P.F.;
"Charcot-Marie-Tooth neuropathy type 1B is associated with mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96432254; PubMed=8835320; Blanquet-Grossard F., Pham-Dinh D., Dautigny A., Latour P., Bannebouche C., Corbillon E., Chazot G., Vandenberghe A.; Charcot-Marie-Tooth type 1B neuropathy: third mutation of serine 63 codon in the major peripheral myelin glycoprotein PO gene."; Clin. Genet. 48:281-283(1995).
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Su.Y., Brooks D.G., Li L., Lepercq J., Trofatter J.A., Ravetch J.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nelis B., Timmerman V., de Jonghe P., Vandenberghe A., Pham-Dinh D., Dautigny A., Martin J.J., van Broeckhoven C., "Rapid screening of myelin genes in CMT1 patients by SSCP analysis: identification of new mutations and polymorphisms in the PO gene.";
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"Mutations in the peripheral myelin genes and associated genes in
inherited peripheral neuropathies.";
                                                                                                             MEDLINE=94061030; PubMed=7694726;
Hayasaka K., Takada G., Ionasescu V.V.;
"Mutation of the myelin P0 gene in Charcot-Marie-Tooth neuropathy
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Latour P., Blanquet F., Nelis E., Bonnebouche C., Chapon F.,
Diraison P., Ollagnon E., Dautigny A., Pham-Dinh D., Chazot G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Myelin protein zero gene mutated in Charcot-Marie-Tooth type
                                                                                                                                                                                                                                VARIANT CMTIB CYS-82.
MEDLINE=94083941; PubMed=7505151;
Himoro M., Yoshikawa H., Marsui T., Mitsui Y., Takahashi M., Kaido M., Nishimura T., Sawaishi Y., Takada G., Hayasaka K.; "New mutation of the myelin P0 gene in a pedigree of Charcot-Marie-Tooth neuropathy 1.";
Biochem. Mol. Biol. Int. 31:169-173(1993).
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                                                                                                                                                                                               Mol. Genet. 2:1369-1372(1993).
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MEDLINE=95080774; PubMed=7527371;
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MEDLINE=94035113; PubMed=7693129;
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MEDLINE=94100981; PubMed=7506095;
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                                                           Mutat. 13:11-28(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the myelin PO gene.";
Nat. Genet. 5:31-34(1993).
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129 KAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTE-VKHVTKVEWIFSGRRAKEEIVFRYYH 187
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                                                                                                         MEDLINE=96212920; PubMed=8630052;
Ikegami T., Nicholson G.A., Ikeda H., Ishida A., Johnston H., Wise G.,
Ouvrier R.A., Hayasaka K.;
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Blanquet-Grossard F., Pham-Dinh D., Dautigny A., Latour P.,
Bonnebouche C., Diraison P., Chapon F., Chazot G., Vandenberghe A.;
"Charcot-Marie-Tooth type 1B neuropathy: a mutation at the single
glycosylation site in the major peripheral myelin glycoprotein Po.";
Hum. Mutat. 8:185-186(1996).
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01-JUL-1989 (Rel. 11, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Myelin PO protein (Myelin protein zero) (Myelin peripheral protein)
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
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                                                                                                                                                                                                                                                      VARIANTS CMT1B THR-135 AND SER-137.
MEDLINE=96263736; PubMed=8664899;
MEDLINE=96263736; PubMed=8664899;
Chance P.F., Lupski J.R.;
Chance P.F., Lupski J.R.;
"Myelin protein zero (MPZ) gene mutations in nonduplication type Charcot-Marie-Tooth disease.";
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MEDLINE=81166015; PubMed=2435734;
Sakamoto Y., Kitamura K., Yoshimura K., Nishijima T., Uyemura K.;
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                                                                                                                                                             "A novel homozygous mutation of the myelin Po gene producing
Dejerine-Sottas disease (hereditary motor and sensory neuropathy
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Boucherat M., van Broeckhoven C., Vandenberghe A.; "Mutations in the myelin protein zero gene associated with Charcot-Marie-Tooth disease type 1B.";
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                                                                                                                                                                                                                     Biochem. Biophys. Res. Commun. 222:107-110(1996)
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1 Similarity 26.2%; Pred. No. 0.0011;
45; Conservative 31; Mismatches 74,
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                                                       Hum. Mutat. 6:50-54(1995)
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Best Local 8
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45; Conservative
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179
248
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                                                                                                                                                                                                                                                                                     HSSP; P06907; 1NEU
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P06907;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 KEVHGAVĞSQVTLYCSFWSSEWVSDDLSFTWRYQPEGGRDAİSIFHYAK---GQPYIDEV 63
                                    guides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=91244320; PubMed=1709914; MEDLINE=91244320; PubMed=1709914; You K.H., Haish C.L., Hayes C., Stahl N., Francke U., Popko B.; "UNA sequence, genomic organization, and chromosomal localization of the mouse peripheral myelin protein zero gene: identification of polymorphic alleles.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myelin PO protein precursor (Myelin protein zero) (Myelin peripheral protein) (MPP).
         Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
"Complete amino acid sequence of PO protein in bovine peripheral
                                                                                                                                                                                                                                                                                                                                                                  . .) (COMPLEX)
                                                                                       Schwann cells.
-!- PTM: N-GLYCAN IS SULFATED.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Belongs to the myelin P0 protein family.
                                                                                                                                       PIR; A2012.

HSSP; P06907; 1NEU.

GlycosuiteDB; P10522.

InterPro; IPR00110; Ig-like.

InterPro; IPR003596; Ig-v.

InterPro; IPR003596; Ig-v.

InterPro; IPR003596; Ig-v.

InterPro; IPR00359; Myelin P0.

RNANT; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 1.

PROSITE; PS50836; MYELIN P0; 1.

PROSITE; PS0568; MYELIN P0; 1.

Myelin; Structural proteIn; Glycoprotein; Transmembrane;

Phosphorylation; Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           PKC).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258 TLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVK 297
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                                                                                                                                                                                                                                                                                                                                                                    (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 131; DB 1;
; Pred. No. 0.0011;
27; Mismatches 7;
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01-AUG-1992 (Rel. 23, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                        IG-LIKE V-TYPE.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                            181
204
214
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93
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 FRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGNLV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 IFHYAK---GOPYIDEVGAFKERIQWYGDPRWKDGSIVIHNLDYSDNGTFTCDVKNPPDI 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 SLVLSPALAIVVYTD--REIYGAVGSQVTLHCSFWSSEWVSDDISFTWRYQPEGGRDAIS 78
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-!- FUNCTION: Creation of an extracellular membrane face which guides the wrapping process and ultimatelly compacts adjacent lamellae.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SUBCELLULAR FOUND only in peripheral nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-OCT-2003 (Rel. 06, Last sequence update)
Myelin PO protein precursor (Myelin protein zero) (Myelin peripheral protein)
MPS OR PO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20;
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R INTERPROJ IPR00310; Mp2.

R INTERPROJ IPR003596; IG_V.

R INTERPROJ IPR0003296; IG_V.

R RINTS; PR00213; WYELLINPO.

R SMART; SM00406; IGV; 1.

R PROSITE; PS05885; IG_LIKE; 1.

DR PROSITE; PS05685; MYELIN PO; 1.

RW Myelin; Structural protein; Glycoprotein; Transmembrane; KW Phosphorylation; Immunoglobulin domain; Signal.

1 29 BY SIMILARIY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 N-LINKED (GLCNAC. . .) (COMPLEX)
27621 MW; 936D66684300CAC9 CRC64;
                                                                                                                                                                                                                                 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.3%; Score 131; DB 1; Length 248; 25.4%; Pred. No. 0.0014;
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EXTRACELLULAR (BY SIMILARITY)
                                                                                                                                            -!- TLSSUB CELLS.
-!- PTH INTERED GLYCAN IS SULFATED.
-!- PTMILARITY: Contains 1 immunoglobulin-like V-type dom
-!- SIMILARITY: Belongs to the myelin PO protein family.
-!- SIMILARITY: Belongs to the myelin PO protein family.
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32; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M62857; AAA39867.1; JOINED.
M62858; AAA39867.1; JOINED.
M62859; AAA39867.1; JOINED.
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NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --- FUNCTION: Creation of an extracellular membrane face which guides the wrapping process and ultimately compacts adjacent lamellae.
--- SUBCELLULAR LOCATION: Type I membrane protein.
--- TISSUE SPECIFICITY: Found only in peripheral nervous system
                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96413553; PubMed=8816707;
Shapiro L., Doyle J.P., Hensley P., Colman D.R., Hendrickson W.A.;
"Crystal structure of the extracellular domain from P0, the major
structural protein of peripheral nerve myelin.";
                                                                                           Lemke G., Axel R.; "Isolation and sequence of a cDNA encoding the major structural protein of peripheral myelin.";
                                                                                                                                                                                                                                      MEDLINE=90166482; PubMed=2483091;
Lemke G., Lamar E., Patterson J.;
"Isolation and analysis of the gene encoding peripheral myelin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . .) (COMPLEX).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schwann cells.
Schwann cells.
-!- PTM: N-LINKED GLYCAN IS SULFATED.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Belongs to the myelin P0 protein family.
-!- SIMILARITY: Belongs to the myelin point.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; JQ0622; MPRO.
PDB; INEU; 15-MAY-97.
INTERPRO; IPR0071019.
INTERPRO; IPR0070396; Ig-v.
INTERPRO; PR000396; Ig-v.
INTERPRO; PR000920; Myelin_P0.
SMART; SM00406; IGV; I.
PROSITE; PS00568; MGLINPO; I.
Myelin; Structural protein; Glycoprotein; Transmembrane; Phosephorylation; Immunoglobulin domain; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 30-148.
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G -> R (IN DEF ')
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                                                                      MEDLINE=85124601; PubMed=2578885;
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                                                                                                                                                                                                                                                                                                                     protein zero.";
Neuron 1:73-83(1988).
                                                                                                                                                                                              [2]
SEQUENCE FROM N.A.
                                             SEQUENCE FROM N.A.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
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                                                                                                                                                                                                                                                                                                                                 130 AVVLHVLPEEPKELMVHVGGLIQMGCVFQSTE-VKHVTKVEWIFSGRRAKEEIVFRYYHK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                     246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85 ---GQPYIDEVGTFKERIQMVGDPSWKDGSIVIHNLDYSDNGTFTCDVKNPPDIVGKTSQ 141
                                                                                                                                                                                                                                                                                                                                                                                      84
                                                                                                                                                                                                                                                                                                                                                                                                                                   189 LRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGNLVFKKT--
                                                                                                                                                                                                                                                                                                                                                                                29 AIVVYT----DREVYGAVGSQVTLHCSFWSSEWVSDDISFTWRYQPEGGRDAISIFHYAK
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Proc. Natl. Acad. Sci. U.S.A. 94:469-474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

1820WE-6010n carcinoma;

MEDLINE=97165045; Pubmed=9012807;

Heath J.K., White S.J., Johnstone C.N., Catimel B., Simpson R.J.,

Moritz R.L., Tu G.-F., Ji H., Whitehead R.H., Groenen L.C.,

Scott A.M., Ritter G., Cohen L., Welt S., Old L.J., Nice E.C.,

Burgess A.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Characterization of posttranslational modifications of human A33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 IVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97396159; PubMed-9245713;
Ritter G., Cohen L.S., Nice E.C., Catimel B., Burgess A.W.,
Moritz R.L., Ji H., Heath J.K., White S.J., Welt S., Old L.J.,
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                                                                                                                                                                                                                            Length 248;
                                                                                                                                                                                                                      6.3%; Score 130; DB 1; Length 24
25.1%; Pred. No. 0.0016;
ive 32; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Cell surface A33 antigen precursor (Glycoprotein A33).
                                                                                                                                                                               27570 MW; BB703F173466119B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       319 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POST-TRANSLATIONAL MODIFICATIONS
                                                                                                                                                                                                                                                                                 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
107
108
1109
1114
121
130
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                  108
109
112
119
123
138
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MIM;
 14;
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@sib-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 IGR-FONRVHLMGDILCNDGSLLLQDVQEADQGTYICEIR----LKGESQVFKKAVVLHV 135
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10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last sequence update)
X-linked interleukin-1 receptor accessory protein-like 2 precursor (ILIRAPL-2 related protein) (Interleukin-1 receptor 9) (IL-1R9) (IL-1 receptor accessory protein-like 2) (Three immunoglobulin domain-containing IL-1 receptor-related 1) (TIGIRR-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... 
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N-LINKED (GLCNAC. .) (POTENTIAL)
"...wven (GlCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 128.5; DB 1; Length 319;
                                                                                                                          MIM; 602171; -. GO, GO:0005888; C:proteoglycan integral to plasma membrane; GO; GO:0004872; F:receptor activity; TAS. InterPro; IPR007110; Ig-like. InterPro; IPR003596; Ig-v.
                                                                                                                                                                                                                                             SMART; SM00406; ĪGv; 1.
PROSTITE, PSS50835; IG LIKE; 2.
Immunoglobulin domain; Lipoprotein; Palmitate; Glycoprotein;
Trangmembrane; Signal; Antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          310 VLVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEEEFSE 355
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                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL) POTENTIAL.
                                                                                                                                                                                                                                                                                                                                           SURFACE A33 ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51; Mismatches 141;
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IG-LIKE C2-TYPE.
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POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 21.1 nes 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                 Genew; HGNC:4445; GPA33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        261
117
222
211
211
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256
319
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319 AA;
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HUMAN
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A Jin H., Viswesvaraiah R., Gardner R.J., Roberts R.G.;
Jin H., Viswesvaraiah R., Gardner R.J., Roberts R.G.;
Jin H., Viswesvaraiah R., Gardner R.J., Roberts R.G.;

Two novel members of the interleukin-1 receptor gene family, one deleted in Xp21.3-Xp21.3 mental retardation.";

Eur. J. Hum. Genet. 8:87-94(2000).

-!- SUBCELULIAR LOCATION: Type I membrane protein.

-!- SUBCELULIAR LOCATION: Type I membrane protein.

-!- TISSUE SPECIFICITY: Detected at low levels in fetal and adult cerebellum. Detected at very low levels in skin, liver, fetal overy and in placenta.

-!- SIMILARITY: Belongs to the interleukin-1 receptor family.

-!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            class
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"ILIRAPL2 maps to Xq22 and is specifically expressed in the central
nervous System.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification and characterization of two members of a novel clast of the interleukin-1 receptors (IL-IR) family. Delineation of a new class of IL-IR-related proteins based on signaling.";
J. Biol. Chem. 275:29946-29954(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Grabowski M., Lorenz B., Hubel R., Strom T.M.; "A gene (ILIRAPL-2) with 61% identity to ILIRAPL maps to Xq22.2."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                       TISSUE=Fetal brain;
MEDLINE=2044752; PubMed=11031108;
MEDLINE=2044752; PubMed=11031108;
Sana T.R., Debets R., Timans J.C., Bazan J.F., Kastelein R.A.;
Sana T.R., Debets R., Timans J.C., Bazan J.F., Kastelein R.A.;
"Computational identification, cloning, and characterization of
IL-IR9, a novel interleukin-1 receptor-like gene encoded over an
unusually large interval of human chromosome Xq22.2-q22.3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUB=Liver;
MEDLINE=20459050; PubMed=10882729;
Born T.L., Smith D.E., Garka K.E., Renshaw B.R., Bertles J.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM, 300277; ...

MIM, 300277; ...

GO, GO:0004908; F:interleukin-1 receptor activity; TAS.

GO; GO:00074908; F:interleukin-1 receptor activity; TAS.

InterPro; IPR007110; Ig-like.

InterPro; IPR003599; Ig.
                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FROM N.A., AND TISSUE SPECIFICITY.
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115 ICEIRLKGESQVFXKAVVLHVLPEEPKELMVHVGGLIQMGCVFQS----TEVKHVTKVEW 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 LYY----YS---NLSVPIGRFQNRVHLMGDILCN-----DGSLLLQDVQEADQGTY 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 ISCPDMDDFKKSDQEPDVVWYKECKPKM------WRSI------IIQKGNALLIQE 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-LINKED INTERLEUKIN-1 RECEPTOR ACCESSORY PROTEIN-LIKE 2.
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Best Local Similarity 20.3%; Pred. No. 0.0091;
Matches 80; Conservative 60; Mismatches 135; Indels 120; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 3.

IIR.

POTENTIAL.

POTENTIAL.

POTENTIAL.

N-LINKED (GLCNAC. ..) (POTENTIAL).

                                                                                                                  PRINTS, PRO1539; INTRLEUKNIR2.
PRINTS, PRO1539; INTRLEUKNIR2.
PRINTS, PRO1537; INTRLEURIRE.
SMART; SM00409; IG; 2.
SMART; SM0025; TIR; 1.
PROSITE; PS5004; TIR; 1.
PROSITE; PS50104; TIR; 1.
PROSITE; PS
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78669 MW; E400F7ECD186957C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN-LIKE 2.
EXTRACELLULAR (POTENTIAL)
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InterPro, IPR004075; ILI_receptor1.
InterPro, IPR004077; ILI_receptorIIp.
InterPro, IPR000157; TIR.
                                                                           Pfam; PF00047; ig; 3.
Pfam; PF01582; TIR; 1.
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61 PGEHAKDEYVLYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRL 120
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 2067; DB 4; Length 394; Best Local Similarity 100.0%; Pred. No. 3.1e-181; Matches 394; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Foster J.S., Gurney A.L.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AX13996; AAMS2117.1; -.
InterPro; IPR003599; IG.
InterPro; IPR007110; Ig-11ke.
SMART; SM00409; IG; 2.
PROSITE; PS0835; IG LIKE; 2.
SEQUENCE 394 AA; 44339 MW; 64B542F9384C7642 CRC64;
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PRELIMINARY;
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QRn9i7 homo sapien
QZn499 homo sapien
QZn470 homo sapien
QBnf70 homo sapien
QBnf70 homo sapien
Q9ypv4 gallus gall
Q9ypv4 gallus gall
Q9ygh1 gallus gall
Q9ygh1 gallus gall
Q9ygh1 gallus gall
Q9ykv4 homo sapien
Q9rtv4 homo sapien
Q9rtv9 homo sapien
Q9cu80 canis famil
Q9cu80 canis famil
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Q8k100 rattus norv
Q8k100 rattus norv
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1044.657 Million cell updates/sec
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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ALIGNMENTS

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PGEHAKDEYVLYYYSNLSVPIGRFONRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 PGEHAKDEYVLYYYSNLSVPIGRFONRVHLMGDNLCNDGSLLLQDVQEADQGTYICEIRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EPRTLVTPAALRPLVLGGNQLV11VG1VCAT1LLLPVL1L1VKKTCGNKSSVNSTVLVKN 304
                            TKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEATYMTMHPVWPSLRSD 374
                                            DGGNYTCSIHLGNLVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATIL 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLPVLILIVKKTCGNKSSVNSTVLVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREV 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KGESOVFKKAVVLHVLPEEPKELMVHVGGLIOMGCVFOSTEVKHVTKVEWIFSGRRAKEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DGGNYTCSIHLGNLVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNOLVIIVGIVCATIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLPVLILIVKKTCGNKSSVNSTVLVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Potential.
putative junctional adhesion molecule.
B81F99C929D80C53 CRC64;
                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26;
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUB-Bone marrow;
MOGG-Lutz. C., Cave-Riant F., Guibal F.C., Breau M., Di Gioia
Gayre Y.E. C., Lutz B.G.;
"JAML, a novel protein induced in myeloid leukemia cells, has
characteristics of a junctional adhesion molecule.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AJS15553; CADS6620.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IEEEEPSEKSEATYWTWHPVWPSLRSDRNNSLEKKSGGGMPKTQQAF 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IEEEEPSEKSEATYMTMHPVWPSLRSDRNNSLEKKSGGGMPKTQQAF 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                   01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative junctional adhesion molecule precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1783; DB 4;
Pred. No. 3.7e-155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86.3%; Sco...
87.0%; Pred. No. s...
7; Mismatches
                                                                                                                                                                                         Ş
                                                                                                                                                                                         394
                                                                                                                                                                                         PRT;
                                                                                                          RNNSLEKKSGGGMPKTQQAF 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 394 p
394 AA; 43731 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 354; Conservative
                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19
                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
 245
                            315
                                                                                      375
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Q7Z499;
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Q7Z499
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                                                                                      GNKSSVNSTVLVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEAT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRLKGESQVFKKAVVLH 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNLSVPIGRFQNRVHLMGDNLCNDGSLLLQDVQEADQGTYICEIRLKGESQVFKKAVVLH 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLPBEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEBIVFRYYHKLRMSVE 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 VLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVBWIFSGRRAKEEIVFRYYHKLRMSAE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGNLVFKKTIVLHVSPE 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YSOSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGNLVFKKTIVLHVSPE 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVKKTCGNKSSVNSTVLVKN 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
                            GNKSSVNSTVLVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLSFGEHAKDEYVLYYY
               IVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDI FRNDGSIMLQGVRESDGGNYTCSIHLGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DYSLGINDLAVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLSPGEHAKDEYVLYYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                  01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ37080.
Hypothetical protein FLJ37080.
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 96.0%; Score 1985; DB 4; Length 384; Best Local Similarity 99.5%; Pred. No. 1e-173; Matches 378; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C93D8EF6C97E6591 CRC64;
                                                                                                                                                                                       YMTMHPVWPSLRSDRNNSLEKKSGGGMPKTQQAF 394
                                                                                                                                                                                                        YMTMHPVWPSLRSDRNNSLEKKSGGGMPKTQQAF 394
                                                                                                                                                                                                                                                                                          384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    384 AA; 43091 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50835; IG LIKE; 2.
                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein.
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TISSUE=Cerebellum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical
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61 LFSKDKDDASEYVLFYYSNLSVPTGRFQNRSHLVGDTFHNDGSLLLQDVQKADEGIYTCE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                177 AKBEIVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSI 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237 HLGNLVFKKTIVLHVSPEEPRTLVTPAALRPL-----VLGGNQLVIIVGIVCATILLLP 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLILIVKKTCGNKSSVNSTVLVK---NTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREV 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 VLILIVKKAKWNKSSVSSMASVKSLENKEKINP-------EKHIYSSITTWET 342
                                                                                                                                                                                                                                                        1 MICLIKLIVIPVILAPVGYPQGLPGLTVSSPQLRVHVGESVLMGCVVQRTEEKHVDRVDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chretien I., Marcuz A., Courtet M., Katevuo K., Vainio O., Heath J.K., White S.J., Du Pasquier L.;
"CTX, a Xenopus thymocyte receptor, defines a molecular family
                                                                                                                                                                                                                                                                                                                      58 ILSPGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICE
                                                                                                                                                                                                                                  1 MPCPLKLILLPVLL---DYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae;
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78;
                                                                                                                                                                                          34;
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                                                                                                                                                  Length 379;
                                                                                                                                             Query Match 47.5%; Score 982; DB 11; Length 37 Best Local Similarity 56.1%; Pred. No. 1.3e-81; Matches 222; Conservative 35; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
Pfam; PF00047; ig; 2.
SMART; SM00409; IG; 2.
SMART; SM00406; IGc2; 2.
SMART; SM00406; IGv2.
SMART; SM00406; IGv2.
SMART; SM00406; IGv2.
SMOOTHS; PS50835; IG LIKE; 2.
SEQUENCE 379 AA; 42561 MW; 2CC0F2987CB12B7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50835; IG LIKE; 2.
SEQUENCE 335 AA; 36561 MW; 071A313C3CE6DCA0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.6%; Score 198; DB 13; I 22.1%; Pred. No. 1.2e-09; tive 74; Mismatches 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       348 IEEEEPSEKSEATYMTMHPVWPSLRSDRNNSLEKKS 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           343 TERGISGE-SEGTYWTWNPVWPS--SPKASSLVRSS 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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Eur. J. Immunol. 28:4094-4104(1998)
EMBL. AF061023; AAD17523.1; -.
HSSP: P06907; INEU.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99077161; PubMed=9862345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10,
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Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; ig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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ID 09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 IVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205 IVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGN 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 PGEHAKDEYVLYYYSNLSVPIGRFONRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 KGESQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEE 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                    Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.; "The nucleotide sequence of a long cDNA clone isolated from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=B5/EGFP transgenic ICR mice; TISSUE=Trophoblast Stem Cell;
                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.0%; Score 1364; DB 4; Length 283; 99.2%; Pred. No. 7.3e-117; tive 2; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO90409; BAC03390.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR001110; Ig-like.
SMART; SM00409; IG; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 283 AA; 32079 MW; CCACB5B0839EB30E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                    Last sequence update)
Last annotation update)
                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similar to adhesion molecule AMICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 LVFKKTIVLHVSPEEPRTL 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVFKKTIVLHVSPEEPRSI 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, BC050133, AAH50133.1; -...
InterPro; IPR003599; Ig.
InterPro; IPR007110, Ig-like.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003596; Ig_c2.
                 QNNF70;
01-OCT-2002 (TrEMBLrel. 22, Cr
01-OCT-2002 (TrEMBLrel. 22, La
01-OCT-2003 (TrEMBLrel. 25, Le
FLJ00300 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50835; IG_LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 99.21
Matches 257; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                  NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                              TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                   spleen."
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60 FYSAKESQLHTIYYYSEGGSYSYGEFKDR1--TAATSPGNASITISNMQPSDTGSYTCEV 117
                                                                 RL----KGESQVFKKAVVLHVL--PEEP---KELMVHVGGLIQMGCVFQSTEVKHVTKVE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 335 AA; 36553 MW; AA640C5CD02CB16D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               302 TNEQPSADEAAA----PETP--ENDEKHEVQKEETAG 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
CHT1 THYMOCYTE ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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22.1%; Pred. No. 5.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                    EEEEPSEKSEATYMTMHPVWPSLRSDRNNSLEKKSGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ChIl thymocyte antigen precursor.
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InterPro; IPR03596; Ig_v.
Pfam; PF00047; ig, 1.
SMAXT; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Y14063; CAA74390.1; -. HSSP; P06907; INEU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken)
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335
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Les 88; Conserv
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SIGNAL
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Matches
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                                                                                                                                   FYSAKESQLHTIYYYSEQQSYSYGEFKDRI--TAATSPGNASITISNMQPSDTGSYTCEV 117
                                                                                                                                                                                        RL----KGESQVFKKAVVLHVL--PEEP---KELMVHVGGLIQMGCVPQSTEVKHVTKVE 169
                                                                                                                                                                                                                     170 WIFSGRRAKEEIVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQG-VRESD 228
                                                                                                                                                                                                                                                                                                                                                                    229 GGNYTCSIHLGNLVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILL 288
                                                                                                                                                                                                                                                                                                                                                                                                             205 TGHYRCI -- ASNIMGNSTCELDLTSMHSDGNIVAGAL-------IGAILAAVII 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                      289 LPVLILIVKKTCGNKSSVNSTVLVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVI 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----NEENTPOPAVLPSNA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 LSPGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEI 118
                                                               59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59
                                             MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHV--GDSALMGCVFQSTEDKCIFKIDWT
                                                                                                      LSPGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHV--GDSALMGCVFQSTEDKCIFKLDWT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=H.B19; TISSUB=Thymus; STRAIN=H.B19; TISSUB=Thymus; STRAIN=O.; Imhof B.A., Vainio O.; Imhof B.A., Vainio O.; "ChT1, a new IgSF member inhibits thymocyte differentiation at the double positive stage."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.3%; Score 192; DB 13; Length 335; 22.1%; Pred. No. 4.1e-09; ive 76; Mismatches 156; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :.";
to the EMBL/GenBank/DDBJ databases
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335 CHT1 THYMOCYTE ANTIGEN.
36509 MW; AA6159598079B438 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNEQPSADEAAASETP-----ENDEKHEVQKEETAG 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             349 EEEEPSEKSEATYMTMHPVWPSLRSDRNNSLEKKSGGG 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               250 CAIVWVLTKKAKKKKŠSNE-MOVMAQKOSNAEYAOVP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   335 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last seq
(TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ChT1 thymocyte antigen precursor.
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EMBL; Y14064; CAA74391.1; -
HSSP; P06907; 1NEU.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003596; Ig_v.
Ffam; PR00047; ig; 1.
SMART; SM00406, IGv; 1.
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335 AA;
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01-MAY-2000
01-OCT-2003
                                                                                                                                                                                            119
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170 WIFSGRRAKEEIVFRYYHKLRMSVEYSOSWGHFONRVNLVGDIFRNDGSIMLQG-VRESD 228
                                                                                                                                                                                229 GGNYTCSIHLGNLVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILL 288
                                                                                                                                                                                                                                                                                        289 LPVLILIVKKTCGNKSSVNSTVLVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVI 348
                                                                                                                                                                                                                                                                                                                            119 RL----KGESQVFKKAVVLHVL--PEEP----KELMVHVGGLIQMGCVFQSTEVKHVTKVE 169
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                                                                                                             FSPQDDAGQSQ---KSVIVNVLVKPSKPFCKIEGTPEKGHLIYLLCKCDQ-GLPHPT---
                                                                                                                                                                                                                                     205 TGHYRCI -- ASNIMGNSTCELDLTSMHSDGNIVAGAL ------IGAILAAVII
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHV - GDSALMGCVFQSTEDKCIFKIDWT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-RPRL line 0; TISSUE-Thymus;
Katevuo K.H., Boyd R., Gobel T.T., Bean A., Dunon D., Imhof B.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vainto O.; "ChT1, a new IgSF member inhibits thymocyte differentiation double positive stage.", Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 335;
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Oy 296 VKKTCGNKSSVNSTVLVKNTKKTNPEIKERPCHFERCEGEKHIYSPIIVREVIEBEEPSE 355	RESULT 10 QSUKV4 ID QSUKV4 PRELIMINARY; PRT; 344 AA. AC QSUKV4; DT 01-MAY-2000 (TrEMBLrel. 13, Created) DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) DE COXSACKie and adenovirus recebtor protein (Fragment).	GN HCAR2. ON HOMO sapiens (Human). ON Homo sapiens (Human). ON Homo sapiens (Human). ON Homo sapiens (Corraniata; Vertebrata; Euteleostomi; ON Homo sapiens; Eutheria; Primates; Catarrhini; Hominidae; Homo. ON NUBI_TaxID=9606; RN SEQUENCE FROM N.A. RN SEQUENCE FROM N.A. RN MEDLINE=99422053; PubMed=10490761; RN MEDLINE=99422053; PubMed=10490761; RN MEDLINE=99422053; PubMed=10490761; RN ACHORNAL HAACK A., Wang H., Wang X., Eizema K., Pauschinger M., Rechner H., Haack A., Wang H., Houtsmuller A.B., Schultheiss HP., RA Lamers J.M.J., Pollar W.; RA Lamers J.M.J.	RT vector barriers."; RI vector barriers."; RE Gene Ther. (5.1520-1535(1999). RE GO, GO:0004872; F:receptor activity; IEA. DR GO, GO:0004872; F:receptor activity; IEA. DR InterPro; IPR007110; Ig-1ike. DR FAm; PR00047; Ig; 2. DR SMART; SM00408; IGc2; 1. DR PR05ITE; PS58385; IG LIKE; 2. KW Immunoglobulin domain; Receptor. FT NON TER 344 A4; 38097 MW; EEF3722E96C697AA CRC64;	Query Match 8.1%; Score 168; DB 4; Length 344; Best Local Similarity 21.8%; Pred. No. 6.98-07; Matches 87; Conservative 65; Mismatches 148; Indels 100; Gaps 18; Qy 5 LKLILLPVLLDYSLGLNDLNVSPELTYHVGDSALMGCVFQ-STEDKCIFKIDWTLSP 61		Oy 118 IRLKGESQVFKKAVVLHYLPEEPKELMMHVGGILQMGCVFQSTEVKHYTKVENIFS 173 1
QY 170 WIFSGRRAKEEIVPRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQG-VRESD 228	Qy 289 LPVLILIVKKTCGNKSSVNSTVLVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVI 348 1 : : :	RESULT 9 QBWMV3 ID QBWMV3 DT QBWMV3 DT 01-MAR-2002 (TrEMBLrel. 20, Created) DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update) DT 01-MAR-2003 (TrEMBLrel. 20, Last sequence update) DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) DR COXBOOKHE virus and adenovirus receptor BCAR. OS Bos taurus (Bovine). OC Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; OX NCBI TaxID=9913;		0047; ig; 2. 00408; IGC2; 1. 8550835; IGC2; 1. bulin domain; Receptor. 365 AA; 40153 MW; 36DE0BE5DCF88CF9	Query Match 8.9%; Score 183; DB 6; Length 365; Best Local Similarity 23.9%; Pred. No. 3.1e-08; Indels 96; Gaps 20; Matches 95; Conservative 61; Mismatches 146; Indels 96; Gaps 20; Qy 5 LKLILLPVLLDYSLGINDLNVSPPELTVHVQDSALMGCVRQ-STEDKCIFKIDWTLSP 61	0.7 6.2 GEHAKDEYVLYYYSNLSVPIGRFONRVHL-MGDILCNDGSLLLQDVQEADQGTYICE 1.7 1 1 1 1 1 1 1 1 1

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QSTEVKHVTKVEWIFS 173
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--ISVKNASSEYSGTYS 211
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cating anatomical
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ultheiss H.-P.,
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Homo.
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PRELIMINARY;
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ID Q9TU80
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Q9H6B4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 VLHVSPEEPRTLVTP---AALRPLVLGGNQLVI---IVGIVCATIL-LLPVLLLIVKKTC 300
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Placenta;
Crowl R.M., Luk D.;
"Identification of the gene encoding Adlican, a novel protein
stressed in human arthritic tissues.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF245505; AAF86402.1;
HSSP; P56276; ITLK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.1%; Score 167; DB 4; Length 2828;
21.8%; Pred. No. 1.5e-05;
ive 74; Mismatches 149; Indels 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CVFQST--EDKCIFKIDWTLSPG--EHAKD-EYVLYYYSNL-----
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283 PPKSRISTARSY----IGSNHSSLGSMSPSNMEGYSKTQ 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EK--ITAMAGHTISLNCSAAGTPTPSLVWVLPNGTDLQSG 2587
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                                                                                                                                                            01-007-2000 (TrEMBLrel. 15, Created)
01-00T-2000 (TrEMBLrel. 15, Last sequence update)
01-00T-2003 (TrEMBLrel. 25, Last annotation update)
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Homo sapiens (Human)
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87; Conserv
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62 GEHAKDEYVLYYYSNLSVPIGRFQN---RVHL-MGDILCNDGSLLLQDVQEADQGTYICE 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 GRRAKEEIVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYT 233
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STRAIN=breed German shepherd; TISSUE=Liver;
MEDLINE=99422053; PubMed=10490761;
Fechner H., Haack A., Wang H., Wang X., Eizema K., Pauschinger M.,
Schoemaker R.G., van Veghel R., Houtsmuller A.B., Schultheiss H.-P.,
Lamers J.M.J., Poller W.;
"Expression of Coxsackie-adenovirus-receptor and alpha v-integrin does
not correlate with adenovector targeting in vivo indicating anatomical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S LKLILLPVLLDYSLGLNDLNVSPPELTVH--VGDSALMGCVFQ-STEDKCIFKIDWTLSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                      Coxsackie-adenovirus-receptor homolog (Fragment).
Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.9%; Score 164; DB 6; Length 319; Best Local Similarity 22.6%; Pred. No. 1.4e-06; Matches 91; Conservative 61; Mismatches 146; Indels 104;
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                                                                                   Last sequence update)
Last annotation update)
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     319 AA
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                                                        Created)
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                                                  01-MAY-2000 (TrEMBLrel, 13, 01-MAY-2000 (TrEMBLrel, 13, 01-OCT-2003 (TrEMBLrel, 25,
PRELIMINARY;
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Tsuruga H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 HAKDEYVLY----YYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIR 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57
                                                                                                                                         Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S., "NEDO human cDNA sequencing project."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174 GRRAKEEIVFRYYHKLRMSVEYSQSWGHFQ-----NRVNLVGDIFRNDGSIMLQGVRESD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 LKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQ-STEDKCIFKIDWTLSPGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229 GGNYTCSIHLGNLVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.6%; Score 158; DB 4; Length 373;
20.8%; Pred. No. 6.4e-06;
.ive 73; Mismatches 132; Indels 114; Gaps
                                                                                                                                                                                                                                                                                                   Eguchi J., Wada J., Hida K., Zhang H.; "Molecular cloning of adipocyte-specific adhesion molecule (ASAM)."; Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ22415 (Adipocyte-specific adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----ERYE---
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                                                                                                                                                                                                                                                 Strausberg R.; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 NSGRYVWSHVILKVL---VRPSKPKCELEGELTEGSDLTLQCESSS
                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PSS0835; IG'LIKE; 2.
Hypothetical protein; Immunoglobulin domain.
SEQUENCE 373 AA; 41280 MW; FDA215EB3B3C4335 CRC64;
                                                                                                                                                                                                                                                                                                                                        EMBL; AK026068; BAB15347.1;
EMBL; BC009371; AAH09371.1;
EMBL; AY32642; AAP8386.1;
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
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                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; ig; 2.
SMART; SM00408; IGc2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 84; Conserv
                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                     TISSUE=Muscle;
                                                      molecule)
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373 AA

PRT;

PRELIMINARY;

RESULT 14 Q920S5 ID Q920S5

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         270 -----NEIREDAEAPRARLVKPSSSSSGS------RSSRSGSSSTRSTGNSAS 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 DKCIFKIDWTLSPGEHAKDEYVLY----YYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42 EKDTLDİEWLLIDNEGNOKVVITYSSRHVYNNLT---EEQKGRVAFASNFLAGDASLQIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 DVQEADQGTYICEIRLKGE---SQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 TEVKHVTKVEWIFSGRRAKEEIVFRYYHKLRMSVEYSOSWGHF--QNRVNLVGDIFRNDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218 SIMLQGVRESDGGNYTCSIHLGNLVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVI
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Visceral adipose tissue-specific transmembrane protein OL-16.
Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB040490; BAB68503.1; -.
                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 11; Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.5%; Score 154.5; DB 11; Length 21.2%; Pred. No. 1.3e-05; tive 61; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5C6280584AF95326 CRC64;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
dipocyte-specific protein 5.
9030422E11RIK OR ASP5.
Mus musculus (Mouse).
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InterPro; IPR007110; Ig-like.
InterPro; IPR03598; Ig_C2.
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Immunoglobulin domain.
SEQUENCE 373 AA; 41186 MW;
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237 VTGIVAGALLIFLLIWL-
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nes 77; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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| :| :| : | | : | | : | | 143 TEGSDLTLQCESASGTK---PIVY-YWQRIR---EKEGEDEHLPPKSRID-----YNNPG 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 7.4%; Score 152.5; DB 11; Length 372; Best Local Similarity 21.9%; Pred. No. 2e-05; Matches 79; Conservative 61; Mismatches 116; Indels 105; Gaps
STRAIN=OLETP; TISSUE=Visceral adipose;

Hida K., Wada J., Zhang H., Makino H.;
"Molecular cloning of visceral adipose tissue-specific gene.";
"Molecular cloning of visceral adipose tissue-specific gene.";
"Molecular cloning of visceral adipose tissue-specific gene.";
R. Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

R GD, GO:0016021; Cintegral to membrane; IEA.

R InterPro; IPR003199; 19.
R InterPro; IPR003199; 19.
R InterPro; IPR003199; 19.
R Eam; PF00047; 19; 2.
R SMART; SM00409; 169; 1.
R SMART; SM00409; 162; 2.
R SMART; SM00409; 162; 2.
R R SMART; SM00409; 1G2: 1.
R PROSITE; RS50835; 1G_LIKE; 2.
R RMART; CM00409; 1G2. 1.
R ROSOSTE; RS50835; 1G_LIKE; 2.
R RMART; SM00409; 1G2. 1.
R ROSOSTE; RS50835; 1G_LIKE; 2.
R RMART; SM00409; 1G2. 1.
R ROSOSTE; RS50835; 1G_LIKE; 2.
R RMART; SM00409; 1G4. 1.
R RMART; RM00409; 1G6. 1.
R RMAR
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